

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:14:51 ; Search time 36.86 Seconds  
(without alignments)  
213.833 Million cell updates/sec

Title: US-09-202-035-1  
Perfect score: 288  
Sequence: 1 KORQKPPSKPNDPHEFV.....NNPTCWAICKRIPNKKPGKK 49

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/2/paa/PCRUS\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
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  - 10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep.\*
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  - 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*
  - 23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	288	100.0	49	16	US-09-202-035-32
3	288	100.0	49	16	US-09-202-035-36
4	288	100.0	49	16	US-09-202-035-40
5	288	100.0	49	16	US-09-202-035-42
6	288	100.0	49	16	US-09-202-035-43
7	288	100.0	298	23	US-60-208-701-2
8	285	99.0	49	16	US-09-202-035-2
9	285	99.0	49	16	US-09-202-035-3
10	285	99.0	49	16	US-09-202-035-5

11	285	99.0	49	16	US-09-202-035-6	Sequence 6, Appli
12	285	99.0	49	16	US-09-202-035-7	Sequence 7, Appli
13	285	99.0	49	16	US-09-202-035-8	Sequence 8, Appli
14	285	99.0	232	12	US-08-896-442-4	Sequence 4, Appli
15	285	99.0	232	16	US-09-272-262-4	Sequence 4, Appli
16	285	99.0	298	4	US-08-001-534-8	Sequence 8, Appli
17	285	99.0	298	4	US-08-001-534A-8	Sequence 8, Appli
18	285	99.0	298	7	US-08-344-639-8	Sequence 8, Appli
19	285	99.0	298	7	US-08-344-639C-8	Sequence 8, Appli
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21	285	99.0	298	7	US-08-344-639D-8	Sequence 8, Appli
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25	285	99.0	298	8	US-08-467-969-8	Sequence 8, Appli
26	285	99.0	298	12	US-08-834-204-8	Sequence 8, Appli
27	285	99.0	298	12	US-08-838-189-8	Sequence 8, Appli
28	285	99.0	298	12	US-08-838-189A-8	Sequence 8, Appli
29	285	99.0	298	12	US-08-838-189B-8	Sequence 8, Appli
30	285	99.0	298	12	US-08-838-189C-8	Sequence 8, Appli
31	285	99.0	298	12	US-08-838-189D-8	Sequence 8, Appli
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34	285	99.0	298	12	US-08-852-344B-8	Sequence 8, Appli
35	285	99.0	298	12	US-08-852-344C-8	Sequence 8, Appli
36	285	99.0	298	12	US-08-896-442-2	Sequence 2, Appli
37	285	99.0	298	16	US-09-272-262-2	Sequence 2, Appli
38	285	99.0	298	16	US-09-479-240-8	Sequence 8, Appli
39	283	98.3	49	16	US-09-202-035-4	Sequence 4, Appli
40	270	93.8	101	18	US/09/462	Sequence 16, Appli
41	267	92.7	101	18	US/09/462	Sequence 15, Appli
42	263	91.3	49	16	US-09-202-035-18	Sequence 18, Appli
43	261	90.6	49	16	US-09-202-035-17	Sequence 17, Appli
44	252	87.5	101	18	US/09/462	Sequence 17, Appli
45	249	86.5	42	16	US-09-202-035-37	Sequence 37, Appli

ALIGNMENTS

RESULT 1  
US-09-202-035-1  
; Sequence 1, Application US/09202035  
; GENERAL INFORMATION:  
; APPLICANT: Jeffrey John Gorman  
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of  
; TITLE OF INVENTION: Respiratory Syncytial Virus  
; FILE REFERENCE: 41585200100  
; CURRENT APPLICATION NUMBER: US/09/202,035  
; EARLIER FILING DATE: 1998-12-17  
; EARLIER APPLICATION NUMBER: PCT/AU97/00351  
; EARLIER FILING DATE: 1997-06-04  
; EARLIER APPLICATION NUMBER: AU PO 0265  
; EARLIER FILING DATE: 1996-06-05  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: respiratory syncytial virus  
US-09-202-035-1

Query Match 100.0%; Score 288; DB 16; Length 49;  
Best Local Similarity 100.0%; Pred. No. 5.8e-27;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KORQKPPSKPNDPHEFVPCISCSNNPTCWAICKRIPNKKPGKK 49  
DB 1 KORQKPPSKPNDPHEFVPCISCSNNPTCWAICKRIPNKKPGKK 49  
RESULT 2



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	Best Local Similarity	100.0%;	Pred. No. 3.7e-26;		
	Matches 49;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Dd	149	KQRKNPPSPNNDFHFEVFNVPSCISCSNPNPTCWAICKRIPNKKPKGKK	197		

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RESULT 10
US-09-202-035-5
; Sequence 5, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; TITLE OF INVENTION: Respiratory Syncytial Virus

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; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202.035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-5

Query Match          99.0%; Score 285; DB 16; Length 49;
Best Local Similarity 98.0%; Pred. No. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 KORQKPPKNPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGKK 49

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US-09-202-035-6
; Sequence 6, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202.035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-6

Query Match          99.0%; Score 285; DB 16; Length 49;
Best Local Similarity 98.0%; Pred. No. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
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US-09-202-035-7
; Sequence 7, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202.035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-7

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Best Local Similarity 98.0%; Pred. No. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
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RESULT 13
US-09-202-035-8
; Sequence 8, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202.035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-8

Query Match          99.0%; Score 285; DB 16; Length 49;
Best Local Similarity 98.0%; Pred. No. 1.3e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGKK 49
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DB 1 KORQKPPKNPNDFHFEVFNFPVCSICSNNTPTCWAICKRIPNKKPGKK 49

RESULT 14
US-08-896-442-4
; Sequence 4, Application US/08896442
; GENERAL INFORMATION:
; APPLICANT: Li, Xiaomao
; APPLICANT: SURYAPRAKESH, Sambhara
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES ENCODING G PROTEIN OF RESPIRATORY
; FILE REFERENCE: 1038-711 MIS
; CURRENT APPLICATION NUMBER: US/08/896,442
; CURRENT FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 232
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-08-896-442-4

Query Match          99.0%; Score 285; DB 12; Length 232;
Best Local Similarity 98.0%; Pred. No. 6.4e-26;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

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RESULT 15
US-09-272-262-4
; Sequence 4, Application US/09272262
; GENERAL INFORMATION:
; APPLICANT: Li, Xiaomao
; APPLICANT: SURYAPRAKESH, Sambhara
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES ENCODING G PROTEIN OF RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS
; FILE REFERENCE: 1038-923 MIS
; CURRENT APPLICATION NUMBER: US/09/272,262
; CURRENT FILING DATE: 1999-03-19
; PRIORITY APPLICATION NUMBER: 08/896,442
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 232
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-272-262-4

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Query Match      99.08; Score 285; DB 16; Length 232;  
Best Local Similarity 98.08; Pred. No. 6.4e-26;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Job time: 80 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: May 21, 2001, 14:14:52 ; Search time 5.53 seconds  
(without alignments)  
62.526 Million cell updates/sec

Title: US-09-202-035-1  
Perfect score: 288  
Sequence: 1 KORQKPPKPNNDHFHFEV.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 41203 seqs, 7056526 residues

Total number of hits satisfying chosen parameters: 41203

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*

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4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pcp.\*  
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6: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	64	22.2	14	5	US-09-654-289-9
4	64	22.2	17	5	US-09-654-289-20
5	61	21.2	17	5	US-09-654-289-19
6	55.5	19.3	1778	1	PCT-US01-04098A-3126
7	55.5	19.3	2099	1	PCT-US01-04098A-1158
8	54	18.8	14	5	US-09-654-289-11
9	53.5	18.6	59	1	PCT-US01-01339-4965
10	52.5	18.2	160	1	PCT-US01-11988-235
11	52.5	18.2	160	5	US-09-833-245-235
12	52	18.1	39	5	US-09-529-027A-9
13	49	17.0	294	1	PCT-US01-03401-12
14	49	17.0	419	1	PCT-US01-03401-14
15	49	17.0	419	5	US-09-549-066-57
16	48.5	16.8	178	1	PCT-US00-35017A-1470
17	48	16.7	67	1	PCT-US01-01351-215
18	48	16.7	79	1	PCT-US01-01339-3915
19	48	16.7	79	1	PCT-US01-01329-1338
20	47.5	16.5	553	5	US-09-430-669-2
21	47.5	16.5	608	5	US-09-803-589-2
22	47.5	16.5	608	5	US-09-803-589-8
23	47.5	16.5	628	1	PCT-US01-06413-5
24	47	16.3	67	1	PCT-US01-01351-221
25	47	16.3	142	1	PCT-US01-04098A-3751
26	47	16.3	471	5	US-09-792-024-88
27	47	16.3	503	6	US-60-248-505-889

28 47 16.3 627 5 US-09-403-661-2 Sequence 2, Appli  
29 47 16.3 627 5 US-09-403-661-4 Sequence 4, Appli  
30 47 16.3 1258 1 PCT-US01-04098A-1117 Sequence 1117, Ap  
31 47 16.3 1299 1 PCT-US01-04098A-1116 Sequence 1116, Ap  
32 47 16.3 1307 1 PCT-US01-04098A-3084 Sequence 3084, Ap  
33 47 16.3 1307 1 PCT-US01-04098A-3085 Sequence 3085, Ap  
34 46.5 16.1 63 1 PCT-US01-03782A-357 Sequence 357, App  
35 46 16.0 36 1 PCT-US00-01979A-264 Sequence 264, App  
36 46 16.0 36 5 US-09-493-795A-264 Sequence 264, App  
37 46 16.0 151 1 PCT-US01-01339-2785 Sequence 2785, Ap  
38 46 16.0 578 1 PCT-US01-04098A-1506 Sequence 1506, Ap  
39 46 16.0 598 1 PCT-US01-04098A-3474 Sequence 3474, Ap  
40 45.5 15.8 415 5 US-09-826-212-6 Sequence 6, Appli  
41 45 15.6 321 5 US-09-739-449-12973 Sequence 12973, A  
42 45 15.6 335 5 US-09-739-449-9014 Sequence 9014, Ap  
43 45 15.6 339 1 PCT-US01-10484-60 Sequence 60, Appl  
44 45 15.6 341 1 PCT-US01-10484-146 Sequence 146, App  
45 45 15.6 371 5 US-09-809-391-481 Sequence 481, App

## ALIGNMENTS

RESULT 1  
US-09-462-816-4  
; Sequence 4, Application US/09462816  
; GENERAL INFORMATION:  
; APPLICANT: LI, Xiaomao  
; APPLICANT: SAMBHARA, Suryaprakash  
; APPLICANT: KLEIN, Michel H.  
; TITLE OF INVENTION: NUCLEIC ACID VACCINES ENCODING G PROTEIN OF RESPIRATORY  
; TITLE OF INVENTION: SYNCYTIAL VIRUS  
; FILE REFERENCE: 1038-1003 MIS:1b  
; CURRENT APPLICATION NUMBER: US/09/462,816  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: PCT/CA98/00697  
; PRIOR FILING DATE: 1998-07-16  
; PRIOR APPLICATION NUMBER: 08/896,442  
; PRIOR FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: respiratory syncytial virus  
US-09-462-816-4

Query Match 99.0%; Score 285; DB 5; Length 232;  
Best Local Similarity 98.0%; Pred. No. 2.3e-27;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPKPNNDHFHFEVFPVCSICSNPTCWAICKRIPNKKPGKK 49  
DB 83 KORQKPPKPNNDHFHFEVFPVCSICSNPTCWAICKRIPNKKPGKK 131

RESULT 2  
US-09-462-816-2  
; Sequence 2, Application US/09462816  
; GENERAL INFORMATION:  
; APPLICANT: LI, Xiaomao  
; APPLICANT: SAMBHARA, Suryaprakash  
; APPLICANT: KLEIN, Michel H.  
; TITLE OF INVENTION: NUCLEIC ACID VACCINES ENCODING G PROTEIN OF RESPIRATORY  
; TITLE OF INVENTION: SYNCYTIAL VIRUS  
; FILE REFERENCE: 1038-1003 MIS:1b  
; CURRENT APPLICATION NUMBER: US/09/462,816  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: PCT/CA98/00697  
; PRIOR FILING DATE: 1998-07-16  
; PRIOR APPLICATION NUMBER: 08/896,442  
; PRIOR FILING DATE: 1997-07-18

# THE UNIVERSITY OF CHICAGO

RESULT 5  
US-09-654-289-19  
Sequence 19, Application US/09654289  
GENERAL INFORMATION:  
APPLICANT: Binz, Hans  
APPLICANT: N'Guyen, Ngoc Thien  
APPLICANT: Baussant, Thierry  
APPLICANT: Trudel, Michel  
TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY  
SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gordon W. Hueschen  
STREET: 715 The "H" Bldg., 310 East Michigan  
CITY: Kalamazoo  
STATE: MI  
COUNTRY: USA  
ZIP: 49007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/654,289  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/721,979  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hueschen, Gordon W.  
REGISTRATION NUMBER: 16,157  
REFERENCE/DOCKET NUMBER: PF57PCTUS/dln  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 616-382-0030  
TELEFAX: 616-382-2030  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: /product= "Orn"  
FEATURE:  
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LOCATION: 16  
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GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.

;; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
;; FILE REFERENCE: 21272-029  
;; CURRENT APPLICATION NUMBER: PCT/US01/04098A  
;; CURRENT FILING DATE: 2001-02-05  
;; PRIOR APPLICATION NUMBER: Not Yet Assigned  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: 09/728,422  
;; PRIOR FILING DATE: 2000-11-30  
;; PRIOR APPLICATION NUMBER: 09/693,325  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 09/663,561  
;; PRIOR FILING DATE: 2000-09-15  
;; PRIOR APPLICATION NUMBER: 09/654,936  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 09/620,325  
;; PRIOR FILING DATE: 2000-07-19  
;; PRIOR APPLICATION NUMBER: 09/598,075  
;; PRIOR FILING DATE: 2000-06-20  
;; PRIOR APPLICATION NUMBER: 09/560,875  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: 09/496,914  
;; PRIOR FILING DATE: 2000-02-03  
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GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.  
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
FILE REFERENCE: 21272-029  
CURRENT APPLICATION NUMBER: PCT/US01/04098A  
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; APPLICANT: Yuan, Junying
; APPLICANT: Miura, Masayuki
; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,066
; FILING DATE: 13-APRIL-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,287B
; FILING DATE: 10-JUN-1994
; APPLICATION NUMBER: US 08/080,850
; FILING DATE: 24-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3920001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; TELEX: 248636 SSK
; INFORMATION FOR SEQ ID NO: 57:
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187	5	10.2	18	1	PCT-US00-09465-8	Sequence 8, Appl
188	5	10.2	18	7	PCT-US99-05606-74	Sequence 74, Appl
189	5	10.2	18	12	US-08-308-887-3	Sequence 3, Appl
190	5	10.2	18	15	US-08-881-094-3	Sequence 3, Appl
191	5	10.2	18	20	US-09-268-992-74	Sequence 74, Appl
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193	5	10.2	21	20	US-09-657-474-74	Sequence 74, Appl
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199	5	10.2	26	23	US-60-192-739-7729	Sequence 7729, Ap
200	5	10.2	26	23	US-60-194-243-1947	Sequence 1947, Ap
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202	5	10.2	32	6	PCT-US96-01056-36	Sequence 36, Appl
203	5	10.2	32	7	US-08-284-391A-46	Sequence 46, Appl
204	5	10.2	32	7	US-08-394-176-36	Sequence 36, Appl
205	5	10.2	32	7	US-08-394-388A-46	Sequence 46, Appl
206	5	10.2	32	8	US-08-488-18A-35	Sequence 35, Appl
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208	5	10.2	32	16	US-09-218-980-46	Sequence 46, Appl
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211	5	10.2	37	23	US-60-171-489-929	Sequence 929, Ap
212	5	10.2	41	23	US-60-141-862-594	Sequence 694, Ap
213	5	10.2	43	1	PCT-US99-01621-181	Sequence 181, Ap
214	5	10.2	43	17	US-09-363-044A-185	Sequence 185, Ap
215	5	10.2	43	23	US-60-160-203-6341	Sequence 6341, Ap
216	5	10.2	43	23	US-60-160-203-6341	Sequence 6341, Ap
217	5	10.2	43	23	US-60-169-840-6899	Sequence 6899, Ap
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219	5	10.2	46	17	US-09-369-247-112	Sequence 112, Ap
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226	5	10.2	50	23	US-60-170-374-3246	Sequence 3246, Ap
227	5	10.2	50	23	US-60-182-076-361	Sequence 361, Ap
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229	5	10.2	50	23	US-60-198-828-915	Sequence 915, Ap

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232	5	10.2	52	1	PCT-US01-01330-154	Sequence 154, App	305	5	10.2	74	23	US-60-160-209-3591	Sequence 3591, App
233	5	10.2	53	16	US-09-270-767-33307	Sequence 33307, A	306	5	10.2	74	23	US-60-192-739-3815	Sequence 3815, App
234	5	10.2	53	16	US-09-270-767-48524	Sequence 48524, A	307	5	10.2	74	23	US-60-207-578-15	Sequence 15, App
235	5	10.2	53	23	US-60-160-190-2192	Sequence 2192, App	308	5	10.2	75	1	PCT-US01-01338-1893	Sequence 1893, App
236	5	10.2	53	23	US-60-169-841-2651	Sequence 2651, App	309	5	10.2	75	23	US-60-139-671-254	Sequence 254, App
237	5	10.2	54	16	US-09-270-767-36865	Sequence 36865, A	310	5	10.2	75	23	US-60-140-806-832	Sequence 832, App
238	5	10.2	54	16	US-09-270-767-52082	Sequence 52082, A	311	5	10.2	76	23	US-60-182-802-596	Sequence 596, App
239	5	10.2	54	23	US-60-197-873-2218	Sequence 2218, A	312	5	10.2	77	8	US-08-487-032A-488	Sequence 488, App
240	5	10.2	56	18	US-09-450-969-4539	Sequence 4539, App	313	5	10.2	77	9	US-08-561-469A-488	Sequence 488, App
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245	5	10.2	58	23	US-60-178-308-2049	Sequence 2049, App	318	5	10.2	77	23	US-60-194-508-3103	Sequence 3103, App
246	5	10.2	58	23	US-60-182-568-610	Sequence 610, App	319	5	10.2	78	16	US-09-270-767-57310	Sequence 57310, A
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248	5	10.2	60	16	US-09-252-691C-10379	Sequence 10379, A	321	5	10.2	79	16	US-09-248-796-24012	Sequence 24012, A
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250	5	10.2	60	23	US-60-182-569-1316	Sequence 1316, App	323	5	10.2	79	23	US-60-173-469-1436	Sequence 1436, App
251	5	10.2	61	23	US-60-146-055-567	Sequence 567, App	324	5	10.2	79	23	US-60-173-886-1267	Sequence 1267, App
252	5	10.2	62	19	US-09-540-236-3169	Sequence 3169, App	325	5	10.2	80	1	PCT-US99-22855-1220	Sequence 1220, App
253	5	10.2	62	23	US-60-128-476-4267	Sequence 4267, App	326	5	10.2	80	16	US-09-248-796-23505	Sequence 23505, A
254	5	10.2	62	23	US-60-147-499-6905	Sequence 6905, App	327	5	10.2	80	18	US-09-450-969-5300	Sequence 4468, App
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256	5	10.2	63	23	US-60-170-347-431	Sequence 431, App	329	5	10.2	80	23	US-60-230-845-1474	Sequence 1474, App
257	5	10.2	63	23	US-60-188-162-5046	Sequence 5046, App	330	5	10.2	81	23	US-60-192-887-1190	Sequence 1190, App
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259	5	10.2	64	1	PCT-US99-00108-71	Sequence 71, App	332	5	10.2	82	16	US-09-248-796-22665	Sequence 22665, A
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262	5	10.2	64	21	US-09-739-907-71	Sequence 71, App	335	5	10.2	84	21	US-09-726-643-66	Sequence 66, App
263	5	10.2	65	1	PCT-US93-04128A-14	Sequence 14, App	336	5	10.2	85	16	US-09-270-767-32622	Sequence 32622, A
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267	5	10.2	65	7	US-08-310-503-14	Sequence 14, App	340	5	10.2	85	23	US-09-307-890-647	Sequence 647, App
268	5	10.2	65	23	US-60-236-359-20604	Sequence 20604, A	341	5	10.2	86	17	US-60-163-233-3479	Sequence 3479, App
269	5	10.2	66	16	US-09-270-767-61966	Sequence 61966, A	342	5	10.2	86	23	US-60-170-630-1870	Sequence 1870, App
270	5	10.2	66	23	US-60-160-190-1350	Sequence 1350, App	343	5	10.2	86	23	US-60-138-831-4172	Sequence 4172, App
271	5	10.2	67	1	PCT-US00-00724-635	Sequence 635, App	344	5	10.2	89	23	US-60-162-247-3697	Sequence 3697, App
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274	5	10.2	67	18	US-09-417-507-43356	Sequence 43356, A	347	5	10.2	90	1	PCT-US99-22855-1219	Sequence 1219, App
275	5	10.2	67	20	US-09-699-146-215	Sequence 215, App	348	5	10.2	90	16	US-09-228-886-92	Sequence 92, App
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277	5	10.2	67	23	US-60-160-209-4128	Sequence 4128, App	350	5	10.2	92	23	US-60-192-737-1209	Sequence 1209, App
278	5	10.2	67	23	US-60-162-866-635	Sequence 635, App	351	5	10.2	92	23	US-60-194-106-745	Sequence 745, App
279	5	10.2	67	23	US-60-182-569-1315	Sequence 1315, App	352	5	10.2	93	1	PCT-US00-07725-86	Sequence 86, App
280	5	10.2	67	23	US-60-236-359-19129	Sequence 19129, A	353	5	10.2	93	23	US-60-171-881-1638	Sequence 1638, App
281	5	10.2	68	1	PCT-US00-06049-119	Sequence 119, App	354	5	10.2	94	3	US-07-627-942A-32	Sequence 32, App
282	5	10.2	68	1	PCT-US01-01354-18456	Sequence 18456, A	355	5	10.2	94	3	US-07-627-942A-106	Sequence 106, App
283	5	10.2	68	1	PCT-US99-07885-4	Sequence 4, App	356	5	10.2	94	3	US-07-627-942-32	Sequence 32, App
284	5	10.2	68	18	US-09-288-477-4	Sequence 4, App	357	5	10.2	94	3	US-07-627-942-106	Sequence 106, App
285	5	10.2	68	16	US-09-450-969-5076	Sequence 5076, App	358	5	10.2	95	18	US-09-417-507-34750	Sequence 34750, A
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287	5	10.2	68	23	US-60-143-868-640	Sequence 640, App	360	5	10.2	95	23	US-60-171-494-1319	Sequence 1319, App
288	5	10.2	68	23	US-60-197-873-17938	Sequence 17938, A	361	5	10.2	95	23	US-60-195-136-1558	Sequence 1558, App
289	5	10.2	71	23	US-60-163-233-3080	Sequence 3080, App	362	5	10.2	95	23	US-60-207-359-265	Sequence 265, App
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295	5	10.2	73	15	US-09-120-523-17	Sequence 17, App	368	5	10.2	96	9	US-08-558-658-24	Sequence 24, App
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297	5	10.2	73	18	US-09-453-851A-17	Sequence 17, App	370	5	10.2	96	13	US-08-927-939-47	Sequence 47, App
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299	5	10.2	73	23	US-60-160-203-5728	Sequence 5728, App	372	5	10.2	96	14	US-09-067-447-24	Sequence 24, App
300	5	10.2	73	23	US-60-177-646-2352	Sequence 2352, App	373	5	10.2	96	14	US-09-067-447-24	Sequence 24, App
301	5	10.2	73	23	US-60-187-387-983	Sequence 983, App	374	5	10.2	96	14	US-09-067-447-24	Sequence 24, App
302	5	10.2	74	1	PCT-US01-02723-226	Sequence 226, App	375	5	10.2	96	14	US-09-067-447B-24	Sequence 24, App

376	5	10.2	96	15	US-09-150-813-47	Sequence 47, Appl	449	5	10.2	121	14	US-09-057-963-6	Sequence 6, Appl
377	5	10.2	96	23	US-60-177-646-3965	Sequence 3965, Ap	450	5	10.2	121	14	US-09-057-963A-6	Sequence 6, Appl
378	5	10.2	96	23	US-60-196-174-791	Sequence 791, App	451	5	10.2	121	21	US-09-740-676-7	Sequence 7, Appl
379	5	10.2	97	18	US-09-450-969-5290	Sequence 5290, Ap	452	5	10.2	121	23	US-60-169-867-5209	Sequence 5209, Ap
380	5	10.2	97	23	US-60-196-174-792	Sequence 792, App	453	5	10.2	122	23	US-08-168-091-36	Sequence 36, Appl
381	5	10.2	97	23	US-60-196-718-5229	Sequence 5229, Ap	454	5	10.2	122	8	US-08-483-339-36	Sequence 36, Appl
382	5	10.2	98	23	US-60-171-489-1077	Sequence 1077, Ap	455	5	10.2	122	8	US-08-487-467-36	Sequence 36, Appl
383	5	10.2	98	8	US-08-472-065-188	Sequence 188, App	456	5	10.2	123	19	US-09-583-110-3923	Sequence 3923, Ap
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385	5	10.2	99	18	US-09-417-507-28093	Sequence 28093, A	458	5	10.2	123	23	US-60-196-713-3276	Sequence 3276, Ap
386	5	10.2	99	23	US-60-163-245-2935	Sequence 2935, A	459	5	10.2	124	23	US-60-191-637-33990	Sequence 33990, A
387	5	10.2	99	23	US-60-169-867-6518	Sequence 6518, Ap	460	5	10.2	126	11	US-08-728-742-10	Sequence 10, Appl
388	5	10.2	99	23	US-60-169-868-5465	Sequence 5465, Ap	461	5	10.2	126	11	US-08-728-742A-10	Sequence 10, Appl
389	5	10.2	100	1	PCT-US00-07579-165	Sequence 165, App	462	5	10.2	126	23	US-60-178-308-1719	Sequence 1719, Ap
390	5	10.2	100	1	PCT-US93-09298-36	Sequence 36, Appl	463	5	10.2	127	15	US-09-107-433-8263	Sequence 4763, Ap
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392	5	10.2	100	23	US-60-140-806-892	Sequence 892, App	465	5	10.2	127	23	US-60-194-091-916	Sequence 916, App
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395	5	10.2	101	13	US-08-993-002A-81177	Sequence 81177, Ap	468	5	10.2	129	16	US-09-270-767-42416	Sequence 34216, A
396	5	10.2	101	23	US-60-194-508-2517	Sequence 2517, Ap	469	5	10.2	129	16	US-09-270-767-49433	Sequence 49433, A
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398	5	10.2	103	23	US-60-187-412-450	Sequence 450, App	471	5	10.2	129	23	US-60-196-713-3275	Sequence 3275, Ap
399	5	10.2	104	13	US-08-993-002A-81178	Sequence 81178, Ap	472	5	10.2	131	1	PCT-US00-05881-444	Sequence 444, App
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401	5	10.2	104	16	US-09-270-767-48394	Sequence 48394, A	474	5	10.2	131	16	US-09-270-767-48860	Sequence 48860, A
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404	5	10.2	105	23	US-60-178-308-1718	Sequence 1718, Ap	477	5	10.2	132	1	PCT-US00-00724-110	Sequence 110, App
405	5	10.2	105	23	US-60-192-587-939	Sequence 939, App	478	5	10.2	132	16	US-09-228-986-110	Sequence 110, App
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413	5	10.2	108	23	US-60-147-499-5726	Sequence 5726, App	486	5	10.2	133	8	US-08-467-459-185	Sequence 185, App
414	5	10.2	108	23	US-60-197-873-19256	Sequence 19256, A	487	5	10.2	133	8	US-08-467-459-639	Sequence 639, App
415	5	10.2	109	1	PCT-US93-09298-35	Sequence 35, Appl	488	5	10.2	133	8	US-08-467-602-380	Sequence 380, App
416	5	10.2	109	23	US-60-140-956-2377	Sequence 2377, Ap	489	5	10.2	133	8	US-08-467-602-380	Sequence 380, App
417	5	10.2	110	14	US-09-085-380A-4	Sequence 4, Appl	490	5	10.2	133	8	US-08-468-731-360	Sequence 360, App
418	5	10.2	110	14	US-09-085-380A-4	Sequence 4, Appl	491	5	10.2	133	13	US-08-993-002A-6361	Sequence 6361, Ap
419	5	10.2	110	23	US-60-207-214-490	Sequence 490, App	492	5	10.2	133	13	US-09-270-767-43357	Sequence 43357, A
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421	5	10.2	111	23	US-60-141-863-843	Sequence 843, App	494	5	10.2	133	16	US-09-270-767-58706	Sequence 58706, A
422	5	10.2	112	23	US-60-192-587-942	Sequence 942, App	495	5	10.2	133	23	US-09-417-507-37920	Sequence 37920, A
423	5	10.2	112	23	US-60-194-091-918	Sequence 918, App	496	5	10.2	133	23	US-60-198-693-95	Sequence 55, Appl
424	5	10.2	113	23	US-60-178-308-1720	Sequence 1720, Ap	497	5	10.2	134	8	US-08-467-459-444	Sequence 96, Appl
425	5	10.2	115	1	PCT-US97-02318-297	Sequence 297, App	498	5	10.2	134	8	US-08-467-459-444	Sequence 444, App
426	5	10.2	115	13	US-08-903-470-297	Sequence 297, App	499	5	10.2	134	16	US-09-270-767-34805	Sequence 34805, A
427	5	10.2	116	23	US-60-138-830-288	Sequence 288, App	500	5	10.2	135	16	US-09-270-767-50022	Sequence 50022, A
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429	5	10.2	116	23	US-60-197-873-25119	Sequence 25119, A	502	5	10.2	135	23	US-60-138-831-462	Sequence 33527, A
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431	5	10.2	117	17	US-09-328-352-4998	Sequence 4998, Ap	504	5	10.2	136	23	PCT-US00-05989-607	Sequence 607, App
432	5	10.2	117	23	US-60-142-844-562	Sequence 562, App	505	5	10.2	136	23	US-60-162-247-5067	Sequence 5067, Ap
433	5	10.2	117	23	US-60-177-571-5016	Sequence 5016, Ap	506	5	10.2	136	23	US-60-169-840-9064	Sequence 9064, Ap
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437	5	10.2	119	16	US-09-270-767-58497	Sequence 58497, A	510	5	10.2	138	17	US-09-307-590-443	Sequence 443, App
438	5	10.2	120	1	PCT-US00-02237-32	Sequence 32, App	511	5	10.2	138	17	US-09-328-352-8007	Sequence 8007, Ap
439	5	10.2	120	1	PCT-US00-08983-138	Sequence 138, App	512	5	10.2	139	5	US-08-168-091-35	Sequence 35, Appl
440	5	10.2	120	1	PCT-US00-08983-139	Sequence 139, App	513	5	10.2	139	8	US-08-483-339-35	Sequence 35, Appl
441	5	10.2	120	23	US-60-117-904-6	Sequence 6, Appl	514	5	10.2	139	8	US-08-487-467-35	Sequence 35, Appl
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443	5	10.2	121	8	US-08-482-161-7	Sequence 7, Appl	516	5	10.2	140	23	US-60-194-508-1722	Sequence 1722, Ap
444	5	10.2	121	8	US-08-482-161A-7	Sequence 7, Appl	517	5	10.2	141	23	US-60-196-713-3608	Sequence 3608, Ap
445	5	10.2	121	8	US-08-485-001-7	Sequence 7, Appl	518	5	10.2	141	23	US-60-253-625-2497	Sequence 2497, Ap
446	5	10.2	121	8	US-08-485-001A-7	Sequence 7, Appl	519	5	10.2	141	23	US-60-257-931-3023	Sequence 3023, Ap
447	5	10.2	121	8	US-08-489-666-7	Sequence 7, Appl	520	5	10.2	141	23	US-60-269-308-4045	Sequence 4045, Ap
448	5	10.2	121	8	US-08-489-666A-7	Sequence 7, Appl	521	5	10.2	142	1	PCT-US00-00724-826	Sequence 826, App

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523	5	10.2	142	16	US-09-252-691C-11072	Sequence 11072, A	596	5	10.2	156	8	US-08-467-459A-186	Sequence 186, App
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526	5	10.2	142	23	US-60-173-864-28838	Sequence 28838, A	599	5	10.2	156	8	US-08-467-602-381	Sequence 381, App
527	5	10.2	142	23	US-60-196-713-3606	Sequence 3606, App	600	5	10.2	156	8	US-08-467-602-381	Sequence 381, App
528	5	10.2	142	23	US-60-207-216-556	Sequence 556, App	601	5	10.2	156	8	US-08-468-731-381	Sequence 381, App
529	5	10.2	143	16	US-09-270-767-59852	Sequence 59852, A	602	5	10.2	156	17	US-09-330-360-855	Sequence 855, App
530	5	10.2	143	21	US-09-733-089-3715	Sequence 3715, App	603	5	10.2	156	19	US-09-583-110-5063	Sequence 5063, App
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533	5	10.2	143	23	US-60-140-806-812	Sequence 812, App	606	5	10.2	157	16	US-09-248-796-20649	Sequence 20649, A
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561	5	10.2	147	20	US-09-640-878-99	Sequence 99, App	634	5	10.2	162	18	US-09-450-969-7330	Sequence 7330, App
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565	5	10.2	148	23	US-60-143-993-1662	Sequence 1662, App	638	5	10.2	163	4	US-08-066-3844A-18	Sequence 18, App
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568	5	10.2	149	1	PCT-US01-01348-285	Sequence 285, App	641	5	10.2	164	11	US-08-729-416B-13	Sequence 13, App
569	5	10.2	149	1	PCT-US01-01349-512	Sequence 512, App	642	5	10.2	165	1	PCT-US93-09298-33	Sequence 33, App
570	5	10.2	149	1	PCT-US01-01358-336	Sequence 336, App	643	5	10.2	165	5	US-08-168-091-33	Sequence 33, App
571	5	10.2	149	16	US-09-248-796-17654	Sequence 17654, A	644	5	10.2	165	8	US-08-467-459-427	Sequence 427, App
572	5	10.2	149	16	US-09-270-767-48018	Sequence 48018, A	645	5	10.2	165	8	US-08-467-459-490	Sequence 490, App
573	5	10.2	149	18	US-09-417-507-43616	Sequence 43616, A	646	5	10.2	165	8	US-08-483-339-33	Sequence 33, App
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575	5	10.2	149	23	US-60-196-718-6714	Sequence 6714, App	648	5	10.2	165	12	US-08-827-356-3729	Sequence 3729, App
576	5	10.2	150	21	US-09-733-089-4926	Sequence 4926, App	649	5	10.2	165	20	US-09-611-529-4990	Sequence 4990, App
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579	5	10.2	151	23	US-60-160-402-4015	Sequence 4015, App	652	5	10.2	166	23	US-60-167-17-11921	Sequence 19921, A
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582	5	10.2	152	23	US-60-147-499-4142	Sequence 4142, App	655	5	10.2	166	23	US-60-191-681-15638	Sequence 15638, A
583	5	10.2	152	23	US-60-147-499-4143	Sequence 4143, App	656	5	10.2	167	1	PCT-US00-05883-1068	Sequence 1068, App
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587	5	10.2	154	8	US-60-173-464-20146	Sequence 20146, A	660	5	10.2	168	8	US-09-107-532-3745	Sequence 3745, App
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591	5	10.2	155	21	US-09-733-089-14617	Sequence 14617, A	664	5	10.2	168	19	US-60-128-476-4025	Sequence 4025, App
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593	5	10.2	156	8	US-08-411-295F-306	Sequence 306, App	666	5	10.2	169	18	US-09-417-507-44071	Sequence 44071, A
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669	5	10.2	169	23	US-60-177-662-339	Sequence 339, App	742	5	10.2	185	23	US-60-186-661-539	Sequence 539, App
670	5	10.2	170	1	PCT-US98-25247-339	Sequence 339, App	743	5	10.2	185	23	US-60-190-064-109	Sequence 109, App
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673	5	10.2	170	15	US-09-199-637-339	Sequence 339, App	746	5	10.2	188	8	US-08-467-459-431	Sequence 431, App
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685	5	10.2	173	8	US-08-411-295F-166	Sequence 166, App	758	5	10.2	194	23	US-60-186-652-682	Sequence 682, App
686	5	10.2	173	8	US-08-461-097A-240	Sequence 240, App	759	5	10.2	196	6	US-08-209-2048-244	Sequence 244, App
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695	5	10.2	173	23	US-60-162-866-577	Sequence 577, App	768	5	10.2	196	8	US-08-469-549-254	Sequence 254, App
696	5	10.2	173	23	US-60-194-508-3296	Sequence 3296, Ap	769	5	10.2	196	9	US-08-535-200A-244	Sequence 244, App
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702	5	10.2	174	23	US-60-234-446-1065	Sequence 1065, Ap	775	5	10.2	198	20	US-09-652-758-2	Sequence 2, App11
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704	5	10.2	176	1	PCT-US99-22853B-6222	Sequence 3622, Ap	777	5	10.2	199	8	US-08-467-459-469	Sequence 469, App
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: Sequence 32, Application US/09202035
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: APPLICANT: Jeffrey John Gorman
: TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
: TITLE OF INVENTION: Respiratory Syncytial Virus
: FILE REFERENCE: 415852000100
: CURRENT APPLICATION NUMBER: US/09/202,035
: CURRENT FILING DATE: 1998-12-17
: EARLIER APPLICATION NUMBER: PCT/AU97/00351
: EARLIER FILING DATE: 1997-06-04
: EARLIER APPLICATION NUMBER: AU PO 0265
: EARLIER FILING DATE: 1996-06-05
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 32
: LENGTH: 49
: TYPE: PRT
: ORGANISM: respiratory syncytial virus
US-09-202-035-32

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RESULT      3
US-09-202-035-36
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? TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
? TITLE OF INVENTION: Respiratory Syncytial Virus
? FILE REFERENCE: 415852000100
? CURRENT APPLICATION NUMBER: US/09/202,035
? CURRENT FILING DATE: 1998-12-17
? EARLIER APPLICATION NUMBER: PCT/AU97/00351
? EARLIER FILING DATE: 1997-06-04
? EARLIER APPLICATION NUMBER: AU PO 0265
? EARLIER FILING DATE: 1996-06-05
? NUMBER OF SEQ ID NOS: 44
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RESULT 4  
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; Sequence 40, Application US/09202035  
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; APPLICANT: Jeffrey John Gorman  
; TITLE OF INVENTION: Viral peptides with Structural Homology to Protein G of  
; FILE REFERENCE: 41585200100  
; CURRENT FILING DATE: 1998-12-17  
; EARLIER FILING DATE: 1997-06-04  
; EARLIER APPLICATION NUMBER: PCT/AU97/00351  
; EARLIER FILING DATE: 1997-06-04  
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US-09-202-035-40

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RESULT 5  
US-09-202-035-42

; Sequence 42, Application US/09202035  
; GENERAL INFORMATION:  
; APPLICANT: Jeffrey John Gorman  
; TITLE OF INVENTION: Viral peptides with Structural Homology to Protein G of  
; FILE REFERENCE: 41585200100  
; CURRENT FILING DATE: US/09/202, 035  
; CURRENT FILING DATE: 1998-12-17  
; EARLIER FILING DATE: PCT/AU97/00351  
; EARLIER FILING DATE: 1997-06-04  
; EARLIER APPLICATION NUMBER: AU PO 0265  
; EARLIER FILING DATE: 1996-06-05  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: respiratory syncytial virus  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: benzoyl benzylamide derivatisation  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (49)  
; OTHER INFORMATION: amidation

US-09-202-035-42

Query Match 100.0%; Score 49; DB 16; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-45;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KOROKPPSKPNNDFHFEVFNFPSCISNNPTCWAICKRIRPNKKPGKK 49  
Db 1 KOROKPPSKPNNDFHFEVFNFPSCISNNPTCWAICKRIRPNKKPGKK 49

RESULT 6  
US-09-202-035-43

; Sequence 43, Application US/09202035  
; GENERAL INFORMATION:  
; APPLICANT: Jeffrey John Gorman  
; TITLE OF INVENTION: Viral peptides with Structural Homology to Protein G of  
; FILE REFERENCE: 41585200100  
; CURRENT FILING DATE: US/09/202, 035  
; EARLIER FILING DATE: 1998-12-17  
; EARLIER APPLICATION NUMBER: PCT/AU97/00351  
; EARLIER FILING DATE: 1997-06-04  
; EARLIER APPLICATION NUMBER: AU PO 0265  
; EARLIER FILING DATE: 1996-06-05  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: respiratory syncytial virus  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: biotinyl amide derivatisation  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (49)  
; OTHER INFORMATION: amidation  
US-09-202-035-43

Query Match 100.0%; Score 49; DB 16; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-45;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KOROKPPSKPNNDFHFEVFNFPSCISNNPTCWAICKRIRPNKKPGKK 49  
Db 1 KOROKPPSKPNNDFHFEVFNFPSCISNNPTCWAICKRIRPNKKPGKK 49

RESULT 7  
US-60-208-701-2

; Sequence 2, Application US/60208701  
; GENERAL INFORMATION:  
; APPLICANT: Portner, Allen  
; TITLE OF INVENTION: VACCINE AND GENE THERAPY VECTOR AND METHODS OF USE  
; FILE REFERENCE: 1340-1-030P  
; CURRENT FILING DATE: US/60/208,701  
; CURRENT FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Paramyxoviridae pneumovirinae pneumovirus respiratory syncytial virus  
US-60-208-701-2

Query Match 100.0%; Score 49; DB 23; Length 298;

Best Local Similarity 100.0%; Pred. No. 7.5e-45;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPNKKPKGK 49  
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DB 149 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPNKKPKGK 197

## RESULT 8

US-09-202-035-3  
; Sequence 3, Application US/09202035  
; GENERAL INFORMATION:  
; APPLICANT: Jeffrey John Gorman  
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of  
; FILE REFERENCE: 415852000100  
; CURRENT APPLICATION NUMBER: US/09/202,035  
; EARLIER FILING DATE: 1998-12-17  
; EARLIER APPLICATION NUMBER: PCT/AU97/00351  
; EARLIER FILING DATE: 1997-06-04  
; EARLIER APPLICATION NUMBER: AU PO 0265  
; EARLIER FILING DATE: 1996-06-05  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; TYPE: PRT  
; ORGANISM: respiratory syncytial virus  
US-09-202-035-3

Query Match 98.0%; Score 48; DB 16; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.8e-44;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPNKKPKGK 48  
|||||  
DB 1 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPNKKPKGK 48

## RESULT 9

US-09-202-035-8  
; Sequence 8, Application US/09202035  
; GENERAL INFORMATION:  
; APPLICANT: Jeffrey John Gorman  
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of  
; FILE REFERENCE: 415852000100  
; CURRENT APPLICATION NUMBER: US/09/202,035  
; EARLIER FILING DATE: 1998-12-17  
; EARLIER APPLICATION NUMBER: PCT/AU97/00351  
; EARLIER FILING DATE: 1997-06-04  
; EARLIER APPLICATION NUMBER: AU PO 0265  
; EARLIER FILING DATE: 1996-06-05  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; TYPE: PRT  
; ORGANISM: respiratory syncytial virus  
US-09-202-035-8

Query Match 98.0%; Score 48; DB 16; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.8e-44;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPNKKPKGK 48  
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DB 1 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPNKKPKGK 48

## RESULT 10

US-09-202-035-4  
; Sequence 4, Application US/09202035  
; GENERAL INFORMATION:  
; APPLICANT: Jeffrey John Gorman  
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of  
; FILE REFERENCE: 415852000100  
; CURRENT APPLICATION NUMBER: US/09/202,035  
; EARLIER FILING DATE: 1998-12-17  
; EARLIER APPLICATION NUMBER: PCT/AU97/00351  
; EARLIER FILING DATE: 1997-06-04  
; EARLIER APPLICATION NUMBER: AU PO 0265  
; EARLIER FILING DATE: 1996-06-05  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; TYPE: PRT  
; ORGANISM: respiratory syncytial virus  
US-09-202-035-4

Query Match 93.9%; Score 46; DB 16; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.6e-42;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPNKKPKGK 49  
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DB 4 QNKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIPNKKPKGK 49

## RESULT 11

US-09-202-035-37  
; Sequence 37, Application US/09202035  
; GENERAL INFORMATION:  
; APPLICANT: Jeffrey John Gorman  
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of  
; FILE REFERENCE: 415852000100  
; CURRENT APPLICATION NUMBER: US/09/202,035  
; EARLIER FILING DATE: 1998-12-17  
; EARLIER APPLICATION NUMBER: PCT/AU97/00351  
; EARLIER FILING DATE: 1997-06-04  
; EARLIER APPLICATION NUMBER: AU PO 0265  
; EARLIER FILING DATE: 1996-06-05  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: respiratory syncytial virus  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: acetylation  
; NAME/KEY: SITE  
; LOCATION: (42)  
; OTHER INFORMATION: amidation  
US-09-202-035-37

Query Match 85.7%; Score 42; DB 16; Length 42;  
Best Local Similarity 100.0%; Pred. No. 4.7e-38;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIP 42  
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DB 1 KORONKPPSKPNDHFHEVNFVPCISCSNNPTCMAICKRIP 42

## RESULT 12

US/09/462

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; Sequence 9, Application US/09462918
; GENERAL INFORMATION:
; APPLICANT: PIERRE FABRE MEDICAMENT
; TITLE OF INVENTION: RSV EPITOPES AND ANTIBODIES COMPRISING THEM, USEFUL IN DIAGNOSIS
; FILE REFERENCE: 339188/D17017
; CURRENT APPLICATION NUMBER: US/09/462,918
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: FR 97 09079
; PRIOR FILING DATE: 1997-07-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentln Vers. 2.0
; SEQ ID NO 9
; LENGTH: 43
; TYPE: PRT
; ORGANISM: DERIVATED FROM G PROTEIN OF RSV (RESPIRATORY SYNCYTIAL VIRUS).
; FEATURE:
; OTHER INFORMATION: G8a. The first amino acid residue corresponds to the position aa
US/09/462,918-9
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Query Match          81.6%; Score 40; DB 18; Length 43;
Best Local Similarity 100.0%; Pred. No. 6.9e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 10 KPNDFHEFVFNFPVPCSSNNPTCWAICRIPNKKPGKK 49
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DB 1 KPNDFHEFVFNFPVPCSSNNPTCWAICRIPNKKPGKK 40
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RESULT 13
US-09-202-035-2
; Sequence 2, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-2
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```
Query Match          81.6%; Score 40; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.8e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 10 KPNDFHEFVFNFPVPCSSNNPTCWAICRIPNKKPGKK 49
|||||
DB 10 KPNDFHEFVFNFPVPCSSNNPTCWAICRIPNKKPGKK 49
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```
RESULT 14
US-09-202-035-5
; Sequence 5, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
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; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-5
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Query Match          81.6%; Score 40; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.8e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 10 KPNDFHEFVFNFPVPCSSNNPTCWAICRIPNKKPGKK 49
|||||
DB 10 KPNDFHEFVFNFPVPCSSNNPTCWAICRIPNKKPGKK 49
```

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RESULT 15
US-09-202-035-6
; Sequence 6, Application US/09202035
; GENERAL INFORMATION:
; APPLICANT: Jeffrey John Gorman
; TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
; FILE REFERENCE: 415852000100
; CURRENT APPLICATION NUMBER: US/09/202,035
; CURRENT FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: PCT/AU97/00351
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: AU PO 0265
; EARLIER FILING DATE: 1996-06-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 6
; LENGTH: 49
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-202-035-6
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Query Match          81.6%; Score 40; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.8e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 10 KPNDFHEFVFNFPVPCSSNNPTCWAICRIPNKKPGKK 49
|||||
DB 10 KPNDFHEFVFNFPVPCSSNNPTCWAICRIPNKKPGKK 49
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Search completed: May 21, 2001, 14:18:56
Job time: 114 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 21, 2001, 14:17:17 ; Search time 5.51 Seconds  
(without alignments)  
62.753 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 49

Sequence: 1 KORONKPSKPNNDFFHEVF.....NFTCWAICKRIIPKPKKK 49

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 41203 seqs, 7056526 residues

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Total number of hits satisfying chosen parameters: 41203

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database : Pending\_Patents\_AA\_New:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	81.6	232	5	US-09-462-816-4
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3	6	12.2	304	5	US-09-739-449-9007
4	6	12.2	405	5	US-09-739-449-8921
5	5	10.2	14	5	US-09-654-289-9
6	5	10.2	14	5	US-09-654-289-11
7	5	10.2	17	5	US-09-654-289-19
8	5	10.2	17	5	US-09-654-289-20
9	5	10.2	26	5	US-09-722-329-107
10	5	10.2	36	1	PCT-US00-01979A-264
11	5	10.2	36	5	US-09-493-795A-264
12	5	10.2	50	1	PCT-US01-01321-1293
13	5	10.2	50	1	PCT-US01-01339-3605
14	5	10.2	55	1	PCT-US01-01321-1416
15	5	10.2	74	1	PCT-US01-01339-3043
16	5	10.2	89	1	PCT-US01-01339-3971
17	5	10.2	89	1	PCT-US01-01329-1393
18	5	10.2	96	1	PCT-US01-12305-3
19	5	10.2	126	1	PCT-US01-02732-7
20	5	10.2	165	1	PCT-US01-01339-3994
21	5	10.2	165	1	PCT-US01-01329-1415
22	5	10.2	179	1	PCT-US01-01314-18
23	5	10.2	179	6	US-60-248-505-913
24	5	10.2	196	1	PCT-US01-04098A-3308
25	5	10.2	196	1	PCT-US01-04098A-3309
26	5	10.2	213	1	PCT-US01-01339-3781
27	5	10.2	213	1	PCT-US01-01329-1211

28	5	10.2	220	5	US-09-826-019-58	Sequence 58, App1
29	5	10.2	222	5	US-09-603-124B-450	Sequence 450, App
30	5	10.2	222	5	US-09-603-124B-452	Sequence 452, App
31	5	10.2	235	5	US-09-811-284-150	Sequence 150, App
32	5	10.2	241	5	US-09-773-517-7	Sequence 7, App1
33	5	10.2	241	5	US-09-792-025-7	Sequence 7, App1
34	5	10.2	259	1	PCT-US01-01332-881	Sequence 881, App
35	5	10.2	264	5	US-09-739-449-8702	Sequence 8702, App
36	5	10.2	299	1	PCT-US01-11988-1300	Sequence 1300, App
37	5	10.2	299	1	PCT-US01-11988-1301	Sequence 1301, App
38	5	10.2	299	5	US-09-808-669-6	Sequence 6, App1
39	5	10.2	299	5	US-09-423-844-119	Sequence 119, App
40	5	10.2	299	5	US-09-403-296A-6	Sequence 6, App1
41	5	10.2	299	5	US-09-833-245-1300	Sequence 1300, App
42	5	10.2	299	5	US-09-833-245-1301	Sequence 1301, App
43	5	10.2	299	5	US-09-380-139A-119	Sequence 119, App
44	5	10.2	308	5	US-09-820-019-57	Sequence 57, App1
45	5	10.2	325	5	US-09-510-031-2	Sequence 2, App1
46	5	10.2	325	5	US-09-802-853-4	Sequence 4, App1
47	5	10.2	374	5	US-09-740-288A-12	Sequence 12, App1
48	5	10.2	378	5	US-09-739-449-12692	Sequence 12692, A
49	5	10.2	378	5	US-09-740-288A-33	Sequence 33, App1
50	5	10.2	379	5	US-09-740-288A-26	Sequence 26, App1
51	5	10.2	384	1	PCT-US01-11988-1423	Sequence 1423, App
52	5	10.2	384	5	US-09-833-245-1423	Sequence 1423, App
53	5	10.2	415	5	US-09-740-288A-28	Sequence 28, App1
54	5	10.2	415	5	US-09-739-449-10511	Sequence 10511, A
55	5	10.2	420	5	US-09-773-517-9	Sequence 9, App1
56	5	10.2	420	5	US-09-792-025-9	Sequence 9, App1
57	5	10.2	502	1	PCT-US01-04098A-1166	Sequence 1166, App
58	5	10.2	520	1	PCT-US01-1048A-49	Sequence 49, App1
59	5	10.2	523	1	PCT-US01-04098A-3134	Sequence 3134, App1
60	5	10.2	545	1	PCT-US00-35017A-1139	Sequence 1139, App
61	5	10.2	553	1	US-09-292-862A-2	Sequence 2, App1
62	5	10.2	621	1	PCT-US01-04098A-3646	Sequence 3646, App
63	5	10.2	637	5	US-09-773-517-5	Sequence 5, App1
64	5	10.2	637	5	US-09-792-025-5	Sequence 5, App1
65	5	10.2	658	1	PCT-US01-04098A-1373	Sequence 1373, App
66	5	10.2	669	5	US-09-773-517-1	Sequence 1, App1
67	5	10.2	669	5	US-09-792-025-1	Sequence 1, App1
68	5	10.2	675	5	US-09-773-517-3	Sequence 3, App1
69	5	10.2	675	5	US-09-792-025-3	Sequence 3, App1
70	5	10.2	685	1	PCT-US01-04098A-1763	Sequence 1763, App
71	5	10.2	720	5	US-09-739-449-8512	Sequence 8512, App
72	5	10.2	734	1	PCT-US01-04098A-1341	Sequence 1341, App
73	5	10.2	738	1	PCT-US01-04098A-1340	Sequence 1340, App
74	5	10.2	757	5	US-09-494-297-2	Sequence 2, App1
75	5	10.2	768	5	US-09-773-517-11	Sequence 11, App1
76	5	10.2	768	5	US-09-792-025-11	Sequence 11, App1
77	5	10.2	790	5	US-09-723-153-2	Sequence 2, App1
78	5	10.2	839	5	US-09-739-449-9116	Sequence 9116, App
79	5	10.2	918	1	PCT-US01-04098A-3435	Sequence 3435, App
80	5	10.2	939	1	PCT-US01-04098A-1537	Sequence 1537, App
81	5	10.2	954	1	PCT-US01-04098A-3496	Sequence 3496, App
82	5	10.2	957	1	PCT-US01-04098A-1678	Sequence 1678, App
83	5	10.2	963	1	PCT-US01-04098A-3505	Sequence 3505, App
84	5	10.2	973	1	PCT-US01-11988-1424	Sequence 1424, App
85	5	10.2	973	5	US-09-833-245-1424	Sequence 1424, App
86	5	10.2	999	1	PCT-US01-04098A-1528	Sequence 1528, App
87	5	10.2	1096	1	PCT-US01-04098A-1677	Sequence 1677, App
88	5	10.2	12	1	PCT-US01-11501-235	Sequence 235, App
89	4	8.2	14	6	US-60-283-145-18	Sequence 18, App1
90	4	8.2	15	5	US-09-647-468-126	Sequence 126, App
91	4	8.2	15	5	US-09-647-468-127	Sequence 127, App
92	4	8.2	20	1	PCT-US01-11501-233	Sequence 23, App1
93	4	8.2	20	1	US-09-814-604-73	Sequence 23, App1
94	4	8.2	20	6	US-60-284-797-9	Sequence 9, App1
95	4	8.2	21	5	US-09-815-229-1	Sequence 1, App1
96	4	8.2	24	1	PCT-US01-11988-456	Sequence 456, App
97	4	8.2	24	5	US-09-833-245-456	Sequence 456, App
98	4	8.2	29	5	US-09-813-345-1	Sequence 1, App1
99	4	8.2	30	5	US-09-815-229-16	Sequence 16, App1
100	4	8.2	36	1	PCT-US00-01979A-260	Sequence 260, App

101	4	8.2	36	5	US-09-493-795A-260	Sequence 260, App	174	4	8.2	69	1	PCT-US01-01321-1213	Sequence 1213, Ap
102	4	8.2	37	5	US-09-813-345-3	Sequence 3, Appl1	175	4	8.2	69	5	US-09-345-236B-7	Sequence 7, Appl1
103	4	8.2	37	5	US-09-813-345-4	Sequence 4, Appl1	176	4	8.2	70	1	PCT-US01-11988-1040	Sequence 1040, Ap
104	4	8.2	37	5	US-09-813-345-5	Sequence 5, Appl1	177	4	8.2	70	5	US-09-833-245-1040	Sequence 1040, Ap
105	4	8.2	37	5	US-09-813-345-6	Sequence 6, Appl1	178	4	8.2	71	5	US-09-739-449-8184	Sequence 8184, Ap
106	4	8.2	37	5	US-09-813-345-7	Sequence 7, Appl1	179	4	8.2	73	1	PCT-US01-11988-2161	Sequence 2161, Ap
107	4	8.2	37	5	US-09-813-345-8	Sequence 8, Appl1	180	4	8.2	73	5	US-09-739-449-9323	Sequence 9323, Ap
108	4	8.2	37	5	US-09-813-345-9	Sequence 9, Appl1	181	4	8.2	73	5	US-09-828-769-260	Sequence 260, App
109	4	8.2	37	5	US-09-813-345-10	Sequence 10, Appl	182	4	8.2	73	5	US-09-833-245-2161	Sequence 2161, Ap
110	4	8.2	37	5	US-09-813-345-11	Sequence 11, Appl	183	4	8.2	74	1	PCT-US01-04098A-3714	Sequence 3714, Ap
111	4	8.2	37	5	US-09-813-345-12	Sequence 12, Appl	184	4	8.2	74	1	PCT-US01-04098A-3716	Sequence 3716, Ap
112	4	8.2	37	5	US-09-813-345-13	Sequence 13, Appl	185	4	8.2	74	1	PCT-US01-01305-181	Sequence 181, App
113	4	8.2	39	1	PCT-US01-01335-329	Sequence 329, Appl	186	4	8.2	76	1	PCT-US01-01339-2950	Sequence 2950, Ap
114	4	8.2	39	5	US-09-549-066-46	Sequence 46, Appl	187	4	8.2	76	5	US-09-187-693-36	Sequence 36, Appl
115	4	8.2	40	5	US-09-801-436-300	Sequence 300, Appl	188	4	8.2	76	5	US-09-187-693-37	Sequence 37, Appl
116	4	8.2	40	5	US-09-308-823A-59	Sequence 59, Appl	189	4	8.2	77	6	US-60-248-505-1315	Sequence 1315, Ap
117	4	8.2	42	1	PCT-US01-11988-633	Sequence 633, App	190	4	8.2	78	1	PCT-US01-01339-4526	Sequence 4526, Ap
118	4	8.2	42	1	PCT-US01-11988-635	Sequence 635, App	191	4	8.2	78	1	PCT-US01-01339-1783	Sequence 1783, Ap
119	4	8.2	42	5	US-09-833-245-633	Sequence 633, App	192	4	8.2	81	1	PCT-US01-01339-5105	Sequence 5105, Ap
120	4	8.2	42	5	US-09-833-245-635	Sequence 635, App	193	4	8.2	81	5	US-09-640-211A-831	Sequence 831, App
121	4	8.2	43	5	US-09-601-600-256	Sequence 256, App	194	4	8.2	81	5	US-09-640-211A-1070	Sequence 1070, Ap
122	4	8.2	44	1	PCT-US01-01339-5071	Sequence 5071, Ap	195	4	8.2	82	1	PCT-US01-01339-3247	Sequence 3247, Ap
123	4	8.2	44	1	PCT-US00-35017A-1419	Sequence 1419, Ap	196	4	8.2	82	1	PCT-US01-11988-339	Sequence 339, App
124	4	8.2	44	1	PCT-US01-01321-1429	Sequence 1429, Ap	197	4	8.2	82	5	US-09-833-245-110	Sequence 110, App
125	4	8.2	45	5	US-09-601-600-103	Sequence 103, App	198	4	8.2	82	5	US-09-833-245-339	Sequence 339, App
126	4	8.2	46	5	US-09-809-391-463	Sequence 463, App	199	4	8.2	83	1	PCT-US01-01331-1660	Sequence 1660, Ap
127	4	8.2	47	1	PCT-US01-01339-4066	Sequence 4066, Ap	200	4	8.2	84	1	PCT-US01-01339-5053	Sequence 5053, Ap
128	4	8.2	49	5	PCT-US01-01329-1483	Sequence 1483, Ap	201	4	8.2	84	1	PCT-US01-01339-5152	Sequence 5152, Ap
129	4	8.2	47	1	US-09-640-211A-2118	Sequence 2118, Ap	202	4	8.2	84	1	PCT-US01-11988-1908	Sequence 1908, Ap
130	4	8.2	50	5	PCT-US01-01339-4874	Sequence 4874, Ap	203	4	8.2	84	1	PCT-US01-11988-1909	Sequence 1909, Ap
131	4	8.2	50	5	US-09-739-449-13034	Sequence 13034, A	204	4	8.2	84	5	US-09-833-245-1908	Sequence 1908, Ap
132	4	8.2	51	5	US-09-723-981-3	Sequence 3, Appl1	205	4	8.2	85	1	US-09-833-245-1909	Sequence 1909, Ap
133	4	8.2	52	1	PCT-US01-01339-4441	Sequence 4441, Ap	206	4	8.2	85	1	PCT-US01-01339-4211	Sequence 4211, Ap
134	4	8.2	52	1	PCT-US01-01335-271	Sequence 271, App	207	4	8.2	85	1	PCT-US01-01339-1616	Sequence 1616, Ap
135	4	8.2	52	1	PCT-US01-01329-1698	Sequence 1698, Ap	208	4	8.2	85	5	US-09-739-449-11538	Sequence 11538, A
136	4	8.2	53	5	US-09-640-211A-626	Sequence 626, App	209	4	8.2	86	5	US-09-817-427-367	Sequence 367, App
137	4	8.2	54	1	PCT-US01-01339-5157	Sequence 5157, Ap	210	4	8.2	86	5	US-09-723-981-2	Sequence 2, Appl1
138	4	8.2	54	1	PCT-US01-01339-5211	Sequence 5211, Ap	211	4	8.2	87	1	PCT-US01-01339-4465	Sequence 4465, Ap
139	4	8.2	54	1	PCT-US01-01329-1941	Sequence 1941, Ap	212	4	8.2	87	1	PCT-US01-01339-1722	Sequence 1722, Ap
140	4	8.2	55	5	US-09-815-229-13	Sequence 13, Appl	213	4	8.2	88	5	US-09-739-449-10128	Sequence 10128, A
141	4	8.2	55	1	PCT-US01-11988-882	Sequence 882, App	214	4	8.2	88	5	US-09-739-449-12531	Sequence 12531, A
142	4	8.2	55	1	PCT-US01-01321-1542	Sequence 1542, Ap	215	4	8.2	88	5	US-09-817-427-367	Sequence 367, App
143	4	8.2	55	5	US-09-817-427-323	Sequence 323, App	216	4	8.2	88	5	US-09-833-343-215	Sequence 215, App
144	4	8.2	55	5	US-09-833-245-882	Sequence 882, App	217	4	8.2	89	1	PCT-US01-01350-99	Sequence 99, Appl
145	4	8.2	55	6	US-60-248-505-910	Sequence 910, App	218	4	8.2	89	1	PCT-US01-01339-2989	Sequence 2989, Ap
146	4	8.2	56	1	PCT-US01-01339-3442	Sequence 3442, Ap	219	4	8.2	89	1	PCT-US01-01339-4550	Sequence 4550, Ap
147	4	8.2	56	1	PCT-US01-01339-5018	Sequence 5018, Ap	220	4	8.2	89	1	PCT-US01-11988-1838	Sequence 1838, Ap
148	4	8.2	56	1	PCT-US01-04098A-1746	Sequence 1746, Ap	221	4	8.2	89	1	PCT-US01-01329-1807	Sequence 1807, Ap
149	4	8.2	56	1	PCT-US01-01321-1746	Sequence 1746, Ap	222	4	8.2	89	5	US-09-833-245-1838	Sequence 1838, Ap
150	4	8.2	56	5	US-09-814-666-234	Sequence 234, App	223	4	8.2	90	1	PCT-US01-01339-4289	Sequence 4289, Ap
151	4	8.2	58	1	PCT-US01-01339-3679	Sequence 3679, Ap	224	4	8.2	90	5	US-09-640-211A-1008	Sequence 1008, Ap
152	4	8.2	58	1	PCT-US01-01329-1113	Sequence 1113, Ap	225	4	8.2	91	1	PCT-US01-01339-5013	Sequence 5013, Ap
153	4	8.2	61	5	US-09-640-211A-2340	Sequence 2340, Ap	226	4	8.2	91	1	PCT-US01-01339-5352	Sequence 5352, Ap
154	4	8.2	62	1	PCT-US01-11988-139	Sequence 139, App	227	4	8.2	93	1	PCT-US01-01329-1977	Sequence 1977, Ap
155	4	8.2	62	1	PCT-US01-11988-140	Sequence 140, App	228	4	8.2	93	5	US-09-640-211A-751	Sequence 751, App
156	4	8.2	62	5	US-09-739-449-12601	Sequence 12601, A	229	4	8.2	94	5	US-09-308-828A-449	Sequence 449, App
157	4	8.2	62	5	US-09-833-245-139	Sequence 139, App	230	4	8.2	95	1	PCT-US01-01339-3472	Sequence 3472, Ap
158	4	8.2	62	5	US-09-833-245-140	Sequence 140, App	231	4	8.2	95	1	PCT-US01-01339-5175	Sequence 5175, Ap
159	4	8.2	63	1	PCT-US01-01339-4529	Sequence 4529, Ap	232	4	8.2	95	1	PCT-US01-01321-1058	Sequence 1058, Ap
160	4	8.2	63	1	PCT-US01-04098A-3268	Sequence 3268, Ap	233	4	8.2	95	6	US-60-248-505-1141	Sequence 1141, Ap
161	4	8.2	63	1	PCT-US01-01329-1786	Sequence 1786, Ap	234	4	8.2	96	1	PCT-US01-11988-943	Sequence 943, App
162	4	8.2	63	5	US-09-739-449-12863	Sequence 12863, A	235	4	8.2	96	1	PCT-US01-11988-944	Sequence 944, App
163	4	8.2	65	1	PCT-US00-35017A-989	Sequence 989, App	236	4	8.2	96	1	PCT-US01-01335-281	Sequence 281, App
164	4	8.2	65	5	US-09-739-449-12478	Sequence 12478, A	237	4	8.2	96	5	US-09-308-828A-376	Sequence 376, App
165	4	8.2	66	1	PCT-US01-01350-96	Sequence 96, Appl	238	4	8.2	96	5	US-09-833-245-943	Sequence 943, App
166	4	8.2	67	5	US-09-243-675-10	Sequence 10, Appl	239	4	8.2	96	5	US-09-833-245-944	Sequence 944, App
167	4	8.2	67	5	US-09-243-675-11	Sequence 11, Appl	240	4	8.2	97	1	PCT-US01-01339-3940	Sequence 3940, Ap
168	4	8.2	67	5	US-09-345-236B-47	Sequence 47, Appl	241	4	8.2	97	1	PCT-US01-01339-1363	Sequence 1363, Ap
169	4	8.2	68	1	PCT-US01-01350-118	Sequence 118, App	242	4	8.2	97	1	PCT-US01-01321-901	Sequence 901, App
170	4	8.2	68	1	PCT-US01-11988-1175	Sequence 1175, App	243	4	8.2	97	5	US-09-310-707A-16	Sequence 16, Appl
171	4	8.2	68	1	PCT-US01-01312-885	Sequence 885, App	244	4	8.2	99	1	PCT-US01-01350-109	Sequence 109, App
172	4	8.2	68	1	PCT-US01-01312-1194	Sequence 1194, Ap	245	4	8.2	99	1	PCT-US00-30036A-133	Sequence 133, App
173	4	8.2	68	5	US-09-833-245-175	Sequence 175, App	246	4	8.2	99	1	PCT-US01-11988-720	Sequence 720, App

247	4	8.2	99	1	PCT-US01-04098A-3896	Sequence 3896, Ap	320	4	8.2	119	5	US-09-155-739-12	Sequence 12, Appl
248	4	8.2	99	5	US-09-833-245-720	Sequence 720, App	321	4	8.2	119	5	US-09-155-739-13	Sequence 13, Appl
249	4	8.2	100	1	PCT-US01-04098A-3591	Sequence 3591, Ap	322	4	8.2	120	1	PCT-US01-04098A-1111	Sequence 1121, Ap
250	4	8.2	101	1	PCT-US01-01321-1159	Sequence 1159, Ap	323	4	8.2	120	1	PCT-US01-04098A-3089	Sequence 3089, Ap
251	4	8.2	101	5	US-09-469-200-10	Sequence 10, Appl	324	4	8.2	120	5	US-09-739-449-10718	Sequence 10718, A
252	4	8.2	103	5	US-09-739-449-10710	Sequence 10710, A	325	4	8.2	120	5	US-09-640-211A-2171	Sequence 2171, Ap
253	4	8.2	104	1	PCT-US01-01339-5171	Sequence 5171, Ap	326	4	8.2	121	1	PCT-US01-01339-4538	Sequence 4538, Ap
254	4	8.2	104	5	US-09-147-443D-28	Sequence 28, Appl	327	4	8.2	121	1	PCT-US01-01329-1795	Sequence 1795, Ap
255	4	8.2	105	1	PCT-US01-01310-91	Sequence 91, Appl	328	4	8.2	121	5	US-09-836-377-208	Sequence 208, App
256	4	8.2	105	5	US-09-187-693-40	Sequence 40, Appl	329	4	8.2	122	1	PCT-US00-35017A-1039	Sequence 1039, Ap
257	4	8.2	105	5	US-09-187-693-42	Sequence 42, Appl	330	4	8.2	122	5	US-09-739-449-12725	Sequence 12725, A
258	4	8.2	105	5	US-09-187-693-44	Sequence 44, Appl	331	4	8.2	123	1	PCT-US01-01339-2944	Sequence 2944, Ap
259	4	8.2	105	5	US-09-187-693-50	Sequence 50, Appl	332	4	8.2	123	1	PCT-US01-01339-3559	Sequence 3559, Ap
260	4	8.2	105	5	US-09-187-693-52	Sequence 52, Appl	333	4	8.2	123	5	US-09-640-211A-934	Sequence 934, App
261	4	8.2	105	5	US-09-187-693-54	Sequence 54, Appl	334	4	8.2	123	5	US-09-155-739-11	Sequence 11, Appl
262	4	8.2	105	5	US-09-147-443D-12	Sequence 12, Appl	335	4	8.2	124	5	US-09-646-679-20	Sequence 20, Appl
263	4	8.2	105	5	US-09-147-443D-16	Sequence 16, Appl	336	4	8.2	125	1	PCT-US01-01339-4975	Sequence 4975, Ap
264	4	8.2	105	5	US-09-147-443D-24	Sequence 24, Appl	337	4	8.2	125	1	PCT-US01-01339-2256	Sequence 2256, Ap
265	4	8.2	105	5	US-09-147-443D-52	Sequence 52, Appl	338	4	8.2	125	5	US-09-647-468-159	Sequence 159, App
266	4	8.2	105	5	US-09-147-443D-56	Sequence 56, Appl	339	4	8.2	125	5	US-09-647-468-160	Sequence 160, App
267	4	8.2	105	5	US-09-147-443D-60	Sequence 60, Appl	340	4	8.2	125	5	US-09-833-245-2256	Sequence 2256, Ap
268	4	8.2	105	5	US-09-147-443D-64	Sequence 64, Appl	341	4	8.2	126	1	PCT-US01-01339-4786	Sequence 4786, Ap
269	4	8.2	105	5	US-09-380-910-17	Sequence 17, Appl	342	4	8.2	126	5	US-09-739-449-12059	Sequence 12059, A
270	4	8.2	105	5	US-09-380-910-21	Sequence 21, Appl	343	4	8.2	126	5	US-09-640-211A-2108	Sequence 2108, Ap
271	4	8.2	106	1	PCT-US01-01339-4515	Sequence 4515, Ap	344	4	8.2	126	5	US-09-155-739-2	Sequence 2, Appl1
272	4	8.2	106	1	PCT-US01-01329-1772	Sequence 1772, Ap	345	4	8.2	126	5	US-09-155-739-15	Sequence 15, Appl
273	4	8.2	106	5	US-09-817-427-573	Sequence 573, App	346	4	8.2	127	1	PCT-US01-08117-83	Sequence 83, Appl
274	4	8.2	106	5	US-09-147-443D-4	Sequence 4, Appl1	347	4	8.2	127	5	US-09-647-468-179	Sequence 179, App
275	4	8.2	106	5	US-09-147-443D-8	Sequence 8, Appl1	348	4	8.2	127	5	US-09-647-468-180	Sequence 180, App
276	4	8.2	106	5	US-09-147-443D-20	Sequence 20, Appl	349	4	8.2	127	5	US-09-647-468-181	Sequence 181, App
277	4	8.2	106	5	US-09-147-443D-32	Sequence 32, Appl	350	4	8.2	127	5	US-09-647-468-182	Sequence 182, App
278	4	8.2	106	5	US-09-155-739-5	Sequence 5, Appl1	351	4	8.2	127	5	US-09-640-211A-1151	Sequence 1151, Ap
279	4	8.2	107	1	PCT-US01-01339-5132	Sequence 5132, Ap	352	4	8.2	129	5	US-09-739-449-10612	Sequence 10612, A
280	4	8.2	107	5	US-09-187-693-48	Sequence 48, Appl	353	4	8.2	129	5	US-09-640-211A-772	Sequence 772, App
281	4	8.2	107	5	US-09-380-910-15	Sequence 15, Appl	354	4	8.2	129	5	US-09-640-211A-825	Sequence 825, App
282	4	8.2	107	5	US-09-647-468-93	Sequence 93, Appl	355	4	8.2	130	1	US-09-155-739-45	Sequence 45, Appl
283	4	8.2	107	5	US-09-647-468-99	Sequence 99, Appl	356	4	8.2	130	1	PCT-US01-01339-4534	Sequence 4534, Ap
284	4	8.2	107	5	US-09-647-468-101	Sequence 101, App	357	4	8.2	130	1	PCT-US01-01329-1791	Sequence 1791, Ap
285	4	8.2	107	5	US-09-647-468-107	Sequence 107, App	358	4	8.2	130	1	PCT-US01-01332-803	Sequence 803, App
286	4	8.2	107	5	US-09-647-468-145	Sequence 145, App	359	4	8.2	130	1	PCT-US01-01332-1151	Sequence 1151, Ap
287	4	8.2	107	5	US-09-647-468-146	Sequence 146, Appl	360	4	8.2	131	5	US-09-825-414-58	Sequence 58, Appl
288	4	8.2	107	5	US-09-473-018-1	Sequence 1, Appl1	361	4	8.2	132	1	PCT-US01-04098A-1033	Sequence 1033, Ap
289	4	8.2	107	5	US-09-473-018-3	Sequence 3, Appl1	362	4	8.2	132	5	US-09-473-018-2	Sequence 2, Appl1
290	4	8.2	108	6	US-60-248-505-1292	Sequence 1292, Ap	363	4	8.2	132	5	US-09-473-018-4	Sequence 4, Appl1
291	4	8.2	110	1	PCT-US01-01339-4630	Sequence 4630, Ap	364	4	8.2	132	6	US-60-248-505-997	Sequence 997, App
292	4	8.2	110	1	PCT-US01-01329-1887	Sequence 1887, Ap	365	4	8.2	133	1	PCT-US01-11663-412	Sequence 412, App
293	4	8.2	110	1	US-09-739-449-12521	Sequence 12521, A	366	4	8.2	134	1	PCT-US01-01312-724	Sequence 724, App
294	4	8.2	110	5	US-09-815-229-3	Sequence 3, Appl1	367	4	8.2	134	1	PCT-US01-01332-1128	Sequence 1128, Ap
295	4	8.2	110	5	US-09-602-709-23	Sequence 23, Appl	368	4	8.2	134	1	PCT-US01-01332-926	Sequence 926, App
296	4	8.2	110	5	US-09-602-709-24	Sequence 24, Appl	369	4	8.2	134	1	PCT-US01-01332-1201	Sequence 1201, Ap
297	4	8.2	110	5	US-09-602-709-25	Sequence 25, Appl	370	4	8.2	135	1	PCT-US01-01339-4759	Sequence 4759, Ap
298	4	8.2	110	5	US-09-380-910-12	Sequence 12, Appl	371	4	8.2	135	1	PCT-US01-01312-645	Sequence 645, App
299	4	8.2	111	1	PCT-US01-01339-5127	Sequence 5127, Ap	372	4	8.2	135	5	US-09-640-211A-655	Sequence 655, App
300	4	8.2	111	1	US-09-809-391-673	Sequence 673, App	373	4	8.2	135	5	US-09-640-211A-2137	Sequence 2137, Ap
301	4	8.2	113	1	PCT-US01-11988-1902	Sequence 1902, Ap	374	4	8.2	136	5	US-09-809-391-385	Sequence 385, App
302	4	8.2	113	5	US-09-833-245-1902	Sequence 1902, Ap	375	4	8.2	136	5	US-09-640-211A-2189	Sequence 2189, App
303	4	8.2	114	5	US-09-155-739-43	Sequence 43, Appl	376	4	8.2	138	1	PCT-US01-01339-4396	Sequence 4396, Ap
304	4	8.2	115	1	PCT-US01-04098A-1810	Sequence 1810, Ap	377	4	8.2	138	4	US-08-934-000-11	Sequence 11, Appl
305	4	8.2	115	5	US-09-739-449-11882	Sequence 11882, A	378	4	8.2	138	4	US-08-934-000-13	Sequence 13, Appl
306	4	8.2	115	5	US-09-380-910-3	Sequence 3, Appl1	379	4	8.2	138	4	US-08-934-000-15	Sequence 15, Appl
307	4	8.2	116	1	PCT-US01-11988-544	Sequence 544, App	380	4	8.2	139	4	US-08-934-000-19	Sequence 19, Appl
308	4	8.2	116	5	US-09-833-245-544	Sequence 544, App	381	4	8.2	139	4	US-08-934-000-21	Sequence 21, Appl
309	4	8.2	116	5	US-09-155-739-41	Sequence 41, Appl	382	4	8.2	139	5	US-09-830-160-15	Sequence 15, Appl
310	4	8.2	117	5	US-09-380-910-5	Sequence 5, Appl1	383	4	8.2	141	1	PCT-US01-01339-5220	Sequence 5220, Ap
311	4	8.2	118	1	PCT-US01-04098A-1307	Sequence 1307, Ap	384	4	8.2	141	1	PCT-US01-11663-408	Sequence 408, App
312	4	8.2	118	1	PCT-US00-35017A-938	Sequence 938, App	385	4	8.2	141	1	PCT-US01-01339-1950	Sequence 1950, Ap
313	4	8.2	118	5	US-09-739-449-12760	Sequence 12760, A	386	4	8.2	141	5	US-09-739-449-13274	Sequence 13274, A
314	4	8.2	119	1	PCT-US01-04098A-1623	Sequence 1623, Ap	387	4	8.2	142	1	PCT-US01-01350-87	Sequence 87, Appl
315	4	8.2	119	4	US-08-934-000-78	Sequence 78, Appl	388	4	8.2	142	1	PCT-US00-35017A-1292	Sequence 1292, Ap
316	4	8.2	119	4	US-08-934-000-79	Sequence 79, Appl	389	4	8.2	142	5	US-09-155-739-17	Sequence 17, Appl
317	4	8.2	119	4	US-08-934-000-80	Sequence 80, Appl	390	4	8.2	143	5	US-09-739-449-12748	Sequence 12748, A
318	4	8.2	119	4	US-08-934-000-81	Sequence 81, Appl	391	4	8.2	144	1	PCT-US01-11988-1592	Sequence 1592, Ap
319	4	8.2	119	5	US-09-155-739-10	Sequence 10, Appl	392	4	8.2	144	5	US-09-833-245-1592	Sequence 1592, Ap

393	4	8.2	145	1	PCT-US01-03782A-158	Sequence 158, App	466	4	8.2	190	5	US-09-833-245-692	Sequence 692, App
394	4	8.2	145	1	US-09-640-211A-798	Sequence 798, App	467	4	8.2	193	5	US-09-739-449-10225	Sequence 1025, A
395	4	8.2	147	1	PCT-US01-01339-3988	Sequence 3988, Ap	468	4	8.2	194	1	PCT-US01-01350-155	Sequence 155, App
396	4	8.2	147	1	PCT-US01-01329-1409	Sequence 1409, Ap	469	4	8.2	195	1	PCT-US01-11988-610	Sequence 610, App
397	4	8.2	147	1	US-09-739-449-9554	Sequence 9554, Ap	470	4	8.2	195	1	PCT-US00-3501A-1347	Sequence 1347, Ap
398	4	8.2	148	1	PCT-US01-01339-4077	Sequence 4077, Ap	471	4	8.2	195	5	US-09-833-245-610	Sequence 610, App
399	4	8.2	149	1	PCT-US01-01329-1494	Sequence 1494, Ap	472	4	8.2	195	6	US-60-248-505-1032	Sequence 1032, Ap
400	4	8.2	149	1	PCT-US01-01339-5278	Sequence 5278, Ap	473	4	8.2	197	1	PCT-US01-04098A-1298	Sequence 3298, Ap
401	4	8.2	149	5	US-09-586-875-2	Sequence 2, Appl1	474	4	8.2	197	6	US-60-248-505-942	Sequence 942, App
402	4	8.2	150	5	US-09-822-827-707	Sequence 707, App	475	4	8.2	198	1	PCT-US01-01339-3428	Sequence 3428, Ap
403	4	8.2	151	1	PCT-US01-11663-404	Sequence 404, App	476	4	8.2	198	6	US-60-248-505-1158	Sequence 1158, Ap
404	4	8.2	154	5	US-09-739-449-10411	Sequence 10411, A	477	4	8.2	200	1	PCT-US00-3501A-768	Sequence 768, App
405	4	8.2	155	1	PCT-US01-11988-1804	Sequence 1804, Ap	478	4	8.2	202	1	PCT-US01-11988-1805	Sequence 1805, Ap
406	4	8.2	155	5	US-09-826-019-53	Sequence 53, Appl	479	4	8.2	202	1	PCT-US01-01332-631	Sequence 631, App
407	4	8.2	155	5	US-09-833-245-1804	Sequence 1804, Ap	480	4	8.2	202	5	US-09-739-449-10398	Sequence 10398, A
408	4	8.2	156	1	PCT-US01-01332-885	Sequence 885, App	481	4	8.2	202	5	US-09-828-644-65	Sequence 65, Appl
409	4	8.2	157	1	PCT-US01-01339-4578	Sequence 4578, Ap	482	4	8.2	202	5	US-09-833-245-1805	Sequence 1805, Ap
410	4	8.2	157	1	PCT-US01-01329-1835	Sequence 1835, Ap	483	4	8.2	203	5	US-09-193-5620-3	Sequence 3, Appl1
411	4	8.2	158	5	US-09-640-211A-2167	Sequence 2167, Ap	484	4	8.2	203	6	US-60-248-505-1246	Sequence 1246, Ap
412	4	8.2	159	5	US-09-640-211A-818	Sequence 818, App	485	4	8.2	204	1	PCT-US01-01332-725	Sequence 725, App
413	4	8.2	160	5	US-09-640-211A-699	Sequence 699, App	486	4	8.2	205	5	US-09-461-9208-3	Sequence 3, Appl1
414	4	8.2	162	5	US-09-709-126-10	Sequence 10, Appl	487	4	8.2	206	5	US-09-828-644-116	Sequence 116, App
415	4	8.2	163	1	PCT-US00-35017A-751	Sequence 751, App	488	4	8.2	207	1	PCT-US01-04098A-3410	Sequence 3410, Ap
416	4	8.2	163	1	PCT-US01-01332-952	Sequence 952, App	489	4	8.2	208	5	US-09-823-494-18	Sequence 18, Appl
417	4	8.2	164	5	US-09-739-449-12530	Sequence 12530, A	490	4	8.2	208	6	US-60-248-505-1235	Sequence 1235, Ap
418	4	8.2	164	5	US-09-453-976-12	Sequence 12, Appl	491	4	8.2	210	1	PCT-US00-35017A-802	Sequence 802, App
419	4	8.2	165	5	US-09-722-329-101	Sequence 101, App	492	4	8.2	210	5	US-09-739-449-10470	Sequence 10470, A
420	4	8.2	167	1	PCT-US01-01339-3224	Sequence 3224, Ap	493	4	8.2	210	5	US-09-811-284-229	Sequence 229, App
421	4	8.2	167	1	US-09-453-976-13	Sequence 13, Appl	494	4	8.2	210	6	US-60-248-505-1204	Sequence 1204, Ap
422	4	8.2	167	5	US-09-640-211A-838	Sequence 838, App	495	4	8.2	211	1	PCT-US01-01339-4967	Sequence 4967, Ap
423	4	8.2	168	1	PCT-US01-01312-1019	Sequence 1019, Ap	496	4	8.2	211	1	US-09-739-449-10965	Sequence 10965, A
424	4	8.2	170	1	PCT-US01-01339-3776	Sequence 3776, Ap	497	4	8.2	212	5	US-09-640-211A-796	Sequence 796, App
425	4	8.2	170	1	PCT-US01-01329-1206	Sequence 1206, Ap	498	4	8.2	213	1	PCT-US01-11988-1852	Sequence 1852, Ap
426	4	8.2	171	5	US-09-739-449-11011	Sequence 11011, A	499	4	8.2	213	1	PCT-US01-04098A-1928	Sequence 1928, Ap
427	4	8.2	171	5	US-09-739-449-11614	Sequence 11614, A	500	4	8.2	213	5	US-09-739-449-9632	Sequence 9632, Ap
428	4	8.2	171	6	US-60-248-505-877	Sequence 877, App	501	4	8.2	213	5	US-09-830-135A-59	Sequence 59, Appl
429	4	8.2	172	1	PCT-US00-35017A-1246	Sequence 1246, Ap	502	4	8.2	214	1	PCT-US01-01332-1035	Sequence 1035, Ap
430	4	8.2	172	5	US-09-739-449-11002	Sequence 11002, A	503	4	8.2	215	1	PCT-US01-01332-1004	Sequence 1004, Ap
431	4	8.2	172	5	US-09-640-211A-737	Sequence 737, App	504	4	8.2	215	1	US-09-423-834-59	Sequence 59, Appl
432	4	8.2	174	1	PCT-US00-35017A-1309	Sequence 1309, Ap	505	4	8.2	216	5	US-09-802-706-7	Sequence 7, Appl
433	4	8.2	174	5	US-09-640-211A-768	Sequence 768, App	506	4	8.2	216	5	US-09-822-488-22	Sequence 22, Appl
434	4	8.2	175	5	US-09-739-449-11255	Sequence 11255, A	507	4	8.2	216	5	US-09-830-135A-59	Sequence 59, Appl
435	4	8.2	175	5	US-09-828-644-100	Sequence 100, App	508	4	8.2	217	1	PCT-US01-04098A-1748	Sequence 1748, Ap
436	4	8.2	175	5	US-09-640-211A-774	Sequence 774, App	509	4	8.2	218	5	US-09-739-449-12791	Sequence 12791, A
437	4	8.2	175	6	US-60-248-505-1233	Sequence 1233, Ap	510	4	8.2	218	5	US-09-802-077-9	Sequence 9, Appl1
438	4	8.2	177	6	US-09-739-449-10719	Sequence 10719, A	511	4	8.2	218	5	US-09-792-938-1	Sequence 1, Appl1
439	4	8.2	178	6	US-60-248-505-1332	Sequence 1332, Ap	512	4	8.2	219	1	PCT-US01-01332-832	Sequence 832, App
440	4	8.2	179	5	US-09-739-449-10198	Sequence 10198, A	513	4	8.2	219	1	PCT-US01-01332-1035	Sequence 1035, Ap
441	4	8.2	180	1	PCT-US01-11988-613	Sequence 613, App	514	4	8.2	219	5	US-09-739-449-10548	Sequence 10548, A
442	4	8.2	180	5	US-09-833-245-613	Sequence 613, App	515	4	8.2	220	5	US-09-835-297-4	Sequence 4, Appl1
443	4	8.2	181	1	PCT-US01-11988-910	Sequence 910, App	516	4	8.2	221	1	PCT-US01-04098A-1731	Sequence 1731, Ap
444	4	8.2	181	5	US-09-833-245-910	Sequence 910, App	517	4	8.2	221	1	PCT-US01-01332-766	Sequence 766, App
445	4	8.2	182	1	PCT-US01-11988-1283	Sequence 1283, Ap	518	4	8.2	221	5	US-09-739-449-10626	Sequence 10626, A
446	4	8.2	182	5	US-09-739-449-10021	Sequence 10021, A	519	4	8.2	221	5	US-09-828-644-71	Sequence 71, Appl
447	4	8.2	184	1	US-09-833-245-1283	Sequence 1283, Ap	520	4	8.2	223	1	PCT-US01-01310-63	Sequence 63, Appl
448	4	8.2	184	1	PCT-US01-11988-572	Sequence 572, App	521	4	8.2	223	6	US-60-248-505-807	Sequence 807, App
449	4	8.2	184	1	PCT-US01-11988-1248	Sequence 1248, Ap	522	4	8.2	224	1	PCT-US00-27237-48	Sequence 48, Appl
450	4	8.2	184	1	PCT-US01-11988-1349	Sequence 1349, Ap	523	4	8.2	224	1	PCT-US00-27237-140	Sequence 140, App
451	4	8.2	184	5	US-09-739-449-8804	Sequence 8804, Ap	524	4	8.2	224	5	US-09-828-644-73	Sequence 73, Appl
452	4	8.2	184	5	US-09-833-245-577	Sequence 577, App	525	4	8.2	225	1	PCT-US00-35017A-1020	Sequence 1020, Ap
453	4	8.2	184	5	US-09-833-245-577	Sequence 577, App	526	4	8.2	225	1	PCT-US00-27237-162	Sequence 162, App
454	4	8.2	184	5	US-09-833-245-1248	Sequence 1248, Ap	527	4	8.2	225	1	PCT-US00-27237-164	Sequence 164, App
455	4	8.2	187	5	US-09-833-245-1249	Sequence 1249, Ap	528	4	8.2	225	1	PCT-US00-27237-170	Sequence 170, App
456	4	8.2	187	5	US-09-739-449-12072	Sequence 12072, A	529	4	8.2	225	5	US-09-739-449-10568	Sequence 10568, A
457	4	8.2	188	1	US-09-804-156-17	Sequence 17, Appl	530	4	8.2	226	5	US-09-739-449-9065	Sequence 9065, Ap
458	4	8.2	188	5	PCT-US00-35017A-847	Sequence 847, App	531	4	8.2	226	5	US-09-739-449-9571	Sequence 9571, Ap
459	4	8.2	188	5	US-09-463-891C-36	Sequence 36, Appl	532	4	8.2	227	5	US-09-739-449-8584	Sequence 8584, Ap
460	4	8.2	189	6	US-60-248-505-998	Sequence 998, App	533	4	8.2	228	5	US-09-739-449-8350	Sequence 8350, Ap
461	4	8.2	189	5	PCT-US01-04098A-1330	Sequence 1330, Ap	534	4	8.2	228	5	US-09-821-225-2	Sequence 2, Appl1
462	4	8.2	189	5	US-09-821-803-4	Sequence 4, Appl1	535	4	8.2	229	1	PCT-US01-11988-1483	Sequence 1483, Ap
463	4	8.2	190	1	US-09-828-644-114	Sequence 92, Appl	536	4	8.2	229	1	PCT-US01-11988-1485	Sequence 1485, Ap
464	4	8.2	190	1	PCT-US01-11988-692	Sequence 692, App	537	4	8.2	229	1	PCT-US01-04098A-3798	Sequence 3798, Ap
465	4	8.2	190	5	US-09-640-211A-766	Sequence 766, App	538	4	8.2	229	1	PCT-US01-04098A-3799	Sequence 3799, Ap

539	4	8.2	229	5	US-09-739-449-9020	Sequence 9020, Ap	612	4	8.2	264	1	PCT-US01-10484-163	Sequence 163, App
540	4	8.2	229	5	US-09-828-644-113	Sequence 113, App	613	4	8.2	264	1	PCT-US01-11988-82	Sequence 82, App1
541	4	8.2	229	5	US-09-640-211A-749	Sequence 749, App	614	4	8.2	264	1	PCT-US01-11988-84	Sequence 84, App1
542	4	8.2	229	5	US-09-833-245-1483	Sequence 1483, App	615	4	8.2	264	1	PCT-US01-04098A-3269	Sequence 3269, App
543	4	8.2	229	5	US-09-833-245-1485	Sequence 1485, App	616	4	8.2	264	5	US-09-739-449-13073	Sequence 13073, A
544	4	8.2	230	1	PCT-US01-04098A-1301	Sequence 1301, Ap	617	4	8.2	264	5	US-09-823-494-21	Sequence 21, App
545	4	8.2	232	5	US-09-739-449-10845	Sequence 10845, A	618	4	8.2	264	5	US-09-833-245-82	Sequence 82, App1
546	4	8.2	233	5	US-09-821-255-4	Sequence 4, App1	619	4	8.2	264	5	US-09-833-245-84	Sequence 84, App1
547	4	8.2	234	1	PCT-US01-11988-1191	Sequence 1191, App	620	4	8.2	264	6	US-60-248-505-850	Sequence 850, App
548	4	8.2	234	1	PCT-US01-11988-1322	Sequence 1322, Ap	621	4	8.2	265	5	US-09-709-126-6	Sequence 6, App1
549	4	8.2	234	1	PCT-US01-11988-1803	Sequence 1803, Ap	622	4	8.2	267	5	US-09-826-019-52	Sequence 52, App1
550	4	8.2	234	1	PCT-US01-11988-2210	Sequence 2210, Ap	623	4	8.2	267	5	US-09-826-019-55	Sequence 55, App1
551	4	8.2	234	5	US-09-525-993-7	Sequence 7, App1	624	4	8.2	268	1	PCT-US01-04098A-1166	Sequence 1166, Ap
552	4	8.2	234	5	US-09-833-245-1191	Sequence 1191, Ap	625	4	8.2	269	5	US-09-826-019-100	Sequence 100, App
553	4	8.2	234	5	US-09-833-245-1322	Sequence 1322, Ap	626	4	8.2	269	5	US-09-383-745-3	Sequence 3, App1
554	4	8.2	234	5	US-09-833-245-1803	Sequence 1803, Ap	627	4	8.2	270	5	US-09-739-449-10832	Sequence 10832, A
555	4	8.2	234	5	US-09-833-245-2210	Sequence 2210, Ap	628	4	8.2	270	5	US-09-821-803-6	Sequence 6, App1
556	4	8.2	235	1	PCT-US01-04098A-3355	Sequence 3355, Ap	629	4	8.2	271	1	PCT-US01-04098A-1555	Sequence 1555, Ap
557	4	8.2	235	1	PCT-US00-35017A-845	Sequence 845, App	630	4	8.2	271	1	PCT-US01-01332-650	Sequence 650, App
558	4	8.2	237	1	PCT-US01-01312-727	Sequence 727, App	631	4	8.2	271	5	US-09-739-449-8933	Sequence 8933, Ap
559	4	8.2	237	1	PCT-US01-01332-891	Sequence 891, App	632	4	8.2	272	1	PCT-US01-04098A-3523	Sequence 3523, Ap
560	4	8.2	237	1	PCT-US01-01332-1167	Sequence 1167, App	633	4	8.2	273	1	PCT-US01-01312-968	Sequence 968, App
561	4	8.2	237	5	US-09-828-644-72	Sequence 72, App1	634	4	8.2	273	4	US-08-956-171C-5196	Sequence 5196, Ap
562	4	8.2	238	5	US-09-739-449-13258	Sequence 13258, A	635	4	8.2	273	5	US-09-739-449-9098	Sequence 9098, App
563	4	8.2	239	1	PCT-US01-01312-638	Sequence 638, App	636	4	8.2	273	5	US-09-739-449-9756	Sequence 9756, App
564	4	8.2	240	1	PCT-US01-04098A-1272	Sequence 1272, Ap	637	4	8.2	274	1	PCT-US01-01339-5338	Sequence 5338, Ap
565	4	8.2	240	5	US-09-821-821-4	Sequence 4, App1	638	4	8.2	274	1	PCT-US01-01329-1969	Sequence 1969, App
566	4	8.2	240	5	US-09-821-821-4	Sequence 4, App1	639	4	8.2	275	1	PCT-US01-04098A-3366	Sequence 3366, App
567	4	8.2	241	1	PCT-US01-08518-1	Sequence 1, App1	640	4	8.2	275	5	US-09-739-449-9997	Sequence 23, App1
568	4	8.2	241	5	US-09-822-827-842	Sequence 842, App	641	4	8.2	275	5	US-09-813-408-23	Sequence 23, App1
569	4	8.2	242	1	PCT-US00-35017A-987	Sequence 987, App	642	4	8.2	277	5	US-09-739-449-10900	Sequence 10900, A
570	4	8.2	244	1	PCT-US01-11988-1060	Sequence 1060, App	643	4	8.2	277	5	US-09-336-910A-6	Sequence 6, App1
571	4	8.2	244	5	US-09-833-245-1060	Sequence 1060, App	644	4	8.2	278	5	US-09-810-264-28	Sequence 28, App1
572	4	8.2	247	5	US-09-832-129-57	Sequence 57, App1	645	4	8.2	278	5	US-09-792-024-100	Sequence 100, App
573	4	8.2	248	5	US-09-538-165A-4	Sequence 4, App1	646	4	8.2	280	1	PCT-US01-04098A-3041	Sequence 3041, App
574	4	8.2	249	1	PCT-US01-11988-335	Sequence 335, App	647	4	8.2	280	1	PCT-US01-04098A-3042	Sequence 3042, App
575	4	8.2	249	1	PCT-US01-04098A-1398	Sequence 1398, App	648	4	8.2	280	1	PCT-US01-04098A-3734	Sequence 3734, App
576	4	8.2	249	5	US-09-833-245-335	Sequence 335, App	649	4	8.2	280	1	PCT-US01-01332-814	Sequence 814, App
577	4	8.2	250	5	US-09-739-449-8994	Sequence 8994, App	650	4	8.2	280	5	US-09-823-356-7	Sequence 7, App1
578	4	8.2	250	5	US-09-739-449-10671	Sequence 10671, A	651	4	8.2	282	1	PCT-US00-35017A-1392	Sequence 1392, App
579	4	8.2	251	4	US-08-956-171C-5252	Sequence 5252, App	652	4	8.2	282	1	PCT-US01-01312-782	Sequence 782, App
580	4	8.2	251	5	US-09-739-449-12852	Sequence 12852, A	653	4	8.2	282	5	US-09-739-449-12360	Sequence 12360, A
581	4	8.2	252	1	PCT-US01-11988-2226	Sequence 2226, App	654	4	8.2	284	6	US-60-248-505-06	Sequence 906, App
582	4	8.2	252	5	US-09-833-245-2226	Sequence 2226, App	655	4	8.2	285	5	US-09-739-449-10310	Sequence 10310, A
583	4	8.2	252	6	US-60-248-505-762	Sequence 762, App	656	4	8.2	286	1	PCT-US00-35017A-1425	Sequence 1425, App
584	4	8.2	253	5	US-09-823-494-20	Sequence 20, App1	657	4	8.2	288	1	PCT-US01-04098A-3783	Sequence 3783, App
585	4	8.2	253	6	US-60-248-505-880	Sequence 880, App	658	4	8.2	290	5	US-09-739-449-9480	Sequence 9480, App
586	4	8.2	254	5	US-09-739-449-11499	Sequence 11499, A	659	4	8.2	292	5	US-09-739-449-11557	Sequence 11557, A
587	4	8.2	254	5	US-09-823-494-19	Sequence 19, App1	660	4	8.2	293	5	US-09-739-449-11477	Sequence 11477, A
588	4	8.2	254	5	US-09-823-494-26	Sequence 26, App1	661	4	8.2	293	5	US-09-739-449-11851	Sequence 11851, A
589	4	8.2	254	5	US-09-823-494-28	Sequence 28, App1	662	4	8.2	294	1	PCT-US01-01332-680	Sequence 680, App
590	4	8.2	254	6	US-60-248-505-1033	Sequence 1033, App	663	4	8.2	294	1	PCT-US01-03401-12	Sequence 12, App1
591	4	8.2	255	5	US-09-739-449-12979	Sequence 12979, A	664	4	8.2	295	6	US-60-248-505-1321	Sequence 1321, App
592	4	8.2	255	5	US-09-640-211A-1163	Sequence 1163, App	665	4	8.2	295	5	US-09-739-449-10447	Sequence 10447, A
593	4	8.2	255	5	US-09-640-211A-2261	Sequence 2261, App	666	4	8.2	297	1	PCT-US01-01112-1162	Sequence 1162, App
594	4	8.2	256	1	PCT-US00-35017A-1077	Sequence 1077, App	667	4	8.2	297	5	US-09-739-449-8348	Sequence 8348, App
595	4	8.2	256	5	US-09-739-449-11977	Sequence 11977, A	668	4	8.2	297	5	US-09-097-231-10	Sequence 10, App1
596	4	8.2	256	5	US-09-823-494-22	Sequence 22, App1	669	4	8.2	297	5	US-60-248-505-733	Sequence 733, App
597	4	8.2	256	5	US-09-396-313A-67	Sequence 67, App1	670	4	8.2	298	6	US-09-739-449-9139	Sequence 9139, App
598	4	8.2	257	5	US-09-739-449-12260	Sequence 12260, A	671	4	8.2	298	5	US-09-739-449-11319	Sequence 11319, A
599	4	8.2	257	5	US-09-781-417-82	Sequence 82, App1	672	4	8.2	300	5	US-09-739-449-11339	Sequence 11339, A
600	4	8.2	258	5	US-09-739-449-13173	Sequence 13173, A	673	4	8.2	301	5	US-09-739-449-11943	Sequence 11943, A
601	4	8.2	258	5	US-09-724-400-3	Sequence 3, App1	674	4	8.2	302	6	US-60-248-505-760	Sequence 760, App
602	4	8.2	259	1	PCT-US00-35017A-1062	Sequence 1062, App	675	4	8.2	305	1	PCT-US01-09226-56	Sequence 56, App1
603	4	8.2	259	1	US-09-422-507A-2	Sequence 2, App1	676	4	8.2	305	5	PCT-US01-04098A-1285	Sequence 1285, App
604	4	8.2	260	1	PCT-US01-11988-1021	Sequence 1021, App	677	4	8.2	305	5	US-09-739-449-12821	Sequence 2, App1
605	4	8.2	260	5	US-09-739-449-10363	Sequence 10363, A	678	4	8.2	305	5	US-09-398-583A-2	Sequence 2, App1
606	4	8.2	260	5	US-09-739-449-12252	Sequence 12252, A	679	4	8.2	305	5	US-09-398-583A-4	Sequence 4, App1
607	4	8.2	260	5	US-09-833-245-1021	Sequence 1021, App	680	4	8.2	307	1	PCT-US01-01329-4188	Sequence 4188, App
608	4	8.2	261	1	PCT-US01-10484-160	Sequence 160, App	681	4	8.2	307	1	PCT-US01-01329-1586	Sequence 1586, App
609	4	8.2	261	1	PCT-US01-11988-1020	Sequence 1020, App	682	4	8.2	308	1	PCT-US01-08117-29	Sequence 29, App1
610	4	8.2	261	5	US-09-833-245-1020	Sequence 1020, App	683	4	8.2	308	1	PCT-US01-04098A-1042	Sequence 1042, App
611	4	8.2	263	5	US-09-740-288A-32	Sequence 32, App1	684	4	8.2	308	1	PCT-US01-04098A-3307	Sequence 3307, App

685	4	8.2	309	1	PCT-US01-01332-615	Sequence 615, App	758	4	8.2	348	1	PCT-US01-01332-1068	Sequence 1068, Ap
686	4	8.2	310	1	PCT-US01-04098A-3590	Sequence 3590, Ap	759	4	8.2	349	1	PCT-US01-04098A-3375	Sequence 3375, Ap
687	4	8.2	310	6	US-60-248-505-1265	Sequence 1265, Ap	760	4	8.2	349	1	PCT-US01-01332-956	Sequence 956, App
688	4	8.2	311	5	US-09-538-165A-3	Sequence 3, App1	761	4	8.2	349	1	PCT-US01-12306-5	Sequence 5, App1
689	4	8.2	312	5	US-09-549-066-55	Sequence 55, App1	762	4	8.2	349	5	US-09-343-011A-1	Sequence 1, App1
690	4	8.2	313	5	US-09-739-449-11729	Sequence 11729, A	763	4	8.2	349	5	US-09-826-509-503	Sequence 503, App
691	4	8.2	314	1	PCT-US01-11988-532	Sequence 532, App	764	4	8.2	350	1	PCT-US01-04098A-1738	Sequence 1738, Ap
692	4	8.2	314	5	US-09-739-449-8363	Sequence 8363, App	765	4	8.2	350	1	PCT-US01-01332-635	Sequence 635, App
693	4	8.2	314	5	US-09-739-449-10792	Sequence 10792, A	766	4	8.2	351	5	US-09-830-160-9	Sequence 9, App1
694	4	8.2	314	6	US-09-833-245-592	Sequence 592, App	767	4	8.2	351	5	PCT-US01-04098A-1934	Sequence 1934, Ap
695	4	8.2	315	6	US-60-248-505-849	Sequence 849, App	768	4	8.2	352	5	US-09-739-449-13284	Sequence 13284, A
696	4	8.2	315	1	PCT-US01-01332-758	Sequence 758, App	769	4	8.2	352	5	US-09-761-198-2	Sequence 2, App1
697	4	8.2	315	5	US-09-739-449-9594	Sequence 9594, App	770	4	8.2	353	1	PCT-US00-35017A-1297	Sequence 1297, Ap
698	4	8.2	315	5	US-09-151-771B-10	Sequence 10, App1	771	4	8.2	353	1	PCT-US01-10633-4	Sequence 4, App1
699	4	8.2	316	1	PCT-US01-11944-3	Sequence 3, App1	772	4	8.2	353	5	US-09-739-449-8493	Sequence 8493, Ap
700	4	8.2	316	4	US-08-956-171C-5231	Sequence 5231, Ap	773	4	8.2	360	5	US-09-739-449-12033	Sequence 12033, A
701	4	8.2	318	6	US-09-422-507A-4	Sequence 4, App1	774	4	8.2	360	5	US-09-669-476-2	Sequence 2, App1
702	4	8.2	318	6	US-60-248-505-1122	Sequence 1122, App	775	4	8.2	360	5	US-09-826-509-443	Sequence 443, App
703	4	8.2	320	1	PCT-US00-35017A-1149	Sequence 1149, Ap	776	4	8.2	362	5	US-09-739-449-8416	Sequence 8416, Ap
704	4	8.2	320	6	US-09-811-284-141	Sequence 141, App	777	4	8.2	363	1	PCT-US01-11988-2248	Sequence 2248, Ap
705	4	8.2	320	6	US-60-248-505-1059	Sequence 1059, Ap	778	4	8.2	363	1	PCT-US01-04098A-1030	Sequence 1030, Ap
706	4	8.2	322	5	US-09-806-258-1	Sequence 1, App1	779	4	8.2	363	5	US-09-792-024-80	Sequence 80, App1
707	4	8.2	322	5	US-09-806-258-6	Sequence 6, App1	780	4	8.2	363	5	US-09-832-129-34	Sequence 34, App1
708	4	8.2	323	1	PCT-US01-01339-3635	Sequence 3635, App	781	4	8.2	363	5	US-09-833-245-2248	Sequence 2248, Ap
709	4	8.2	323	1	PCT-US01-01329-1070	Sequence 1070, Ap	782	4	8.2	364	1	PCT-US01-04098A-1071	Sequence 1071, Ap
710	4	8.2	324	1	PCT-US01-01332-692	Sequence 692, App	783	4	8.2	364	4	US-08-706-945B-138	Sequence 138, App
711	4	8.2	325	5	US-09-739-449-12520	Sequence 12520, A	784	4	8.2	364	4	US-08-706-945B-139	Sequence 139, App
712	4	8.2	327	1	PCT-US01-04098A-3253	Sequence 3253, Ap	785	4	8.2	365	1	PCT-US00-35017A-901	Sequence 901, App
713	4	8.2	327	5	US-09-739-449-10789	Sequence 10789, A	786	4	8.2	365	5	US-09-804-006-4	Sequence 4, App1
714	4	8.2	329	5	US-09-739-449-10201	Sequence 10201, A	787	4	8.2	365	5	US-09-804-357-4	Sequence 4, App1
715	4	8.2	329	5	US-09-739-449-10559	Sequence 10559, A	788	4	8.2	366	5	US-09-691-861-2	Sequence 861, App
716	4	8.2	329	5	US-09-336-910A-5	Sequence 5, App1	789	4	8.2	367	5	US-09-739-449-8753	Sequence 8753, Ap
717	4	8.2	329	6	US-60-248-505-1030	Sequence 1030, Ap	790	4	8.2	369	5	US-09-817-183-4	Sequence 2, App1
718	4	8.2	330	6	US-09-739-449-12356	Sequence 12356, A	791	4	8.2	370	1	PCT-US01-04098A-1741	Sequence 1741, Ap
719	4	8.2	331	1	PCT-US01-11988-1917	Sequence 1917, Ap	792	4	8.2	370	5	US-09-739-449-8851	Sequence 8851, Ap
720	4	8.2	331	5	US-09-833-245-1917	Sequence 1917, Ap	793	4	8.2	370	5	US-09-833-790-253	Sequence 253, App
721	4	8.2	332	1	PCT-US01-11945-3	Sequence 3, App1	794	4	8.2	371	5	US-09-739-449-12460	Sequence 12460, A
722	4	8.2	332	1	PCT-US01-01312-1013	Sequence 1013, Ap	795	4	8.2	371	5	US-09-813-408-24	Sequence 24, App1
723	4	8.2	332	6	US-09-097-231-16	Sequence 16, App1	796	4	8.2	373	1	PCT-US01-01312-789	Sequence 789, App
724	4	8.2	332	6	US-60-248-505-1007	Sequence 1007, Ap	797	4	8.2	374	1	PCT-US00-35017A-1064	Sequence 1064, Ap
725	4	8.2	333	5	US-09-739-449-8488	Sequence 8488, Ap	798	4	8.2	374	5	US-09-739-449-11646	Sequence 11646, A
726	4	8.2	334	1	PCT-US01-11988-2164	Sequence 2164, Ap	799	4	8.2	374	5	US-09-820-004-2	Sequence 2, App1
727	4	8.2	334	1	PCT-US01-04098A-3336	Sequence 3336, Ap	800	4	8.2	374	5	US-09-525-993-4	Sequence 4, App1
728	4	8.2	334	5	US-09-833-245-2164	Sequence 2164, Ap	801	4	8.2	376	6	US-60-248-505-1283	Sequence 1283, Ap
729	4	8.2	335	6	US-60-248-505-1215	Sequence 1215, Ap	802	4	8.2	377	1	PCT-US01-04098A-3540	Sequence 3540, Ap
730	4	8.2	336	1	PCT-US01-01332-614	Sequence 614, App	803	4	8.2	377	5	US-09-781-417-81	Sequence 81, App1
731	4	8.2	337	6	US-09-634-656-2	Sequence 2, App1	804	4	8.2	377	5	US-09-740-288A-22	Sequence 22, App1
732	4	8.2	337	6	US-60-248-505-1019	Sequence 1019, Ap	805	4	8.2	377	5	US-09-740-288A-24	Sequence 24, App1
733	4	8.2	337	6	US-60-248-505-1036	Sequence 1036, Ap	806	4	8.2	378	5	US-09-826-509-445	Sequence 445, App
734	4	8.2	338	5	US-09-739-449-10690	Sequence 10690, A	807	4	8.2	378	5	US-09-826-509-445	Sequence 445, App
735	4	8.2	338	5	US-09-723-707-2	Sequence 2, App1	808	4	8.2	381	1	PCT-US00-35017A-1243	Sequence 1243, Ap
736	4	8.2	338	5	US-09-723-707-4	Sequence 4, App1	809	4	8.2	381	5	US-09-739-449-9762	Sequence 9762, A
737	4	8.2	339	1	PCT-US01-11988-2185	Sequence 2185, App	810	4	8.2	382	5	US-09-739-449-12944	Sequence 12944, A
738	4	8.2	339	1	PCT-US01-11988-2185	Sequence 2185, App	811	4	8.2	382	5	US-09-739-449-10482	Sequence 10482, A
739	4	8.2	339	1	PCT-US01-11988-2185	Sequence 2185, App	812	4	8.2	382	6	US-60-248-505-93	Sequence 93, App1
740	4	8.2	339	5	US-09-739-449-11765	Sequence 11765, A	813	4	8.2	383	1	PCT-US01-04098A-3039	Sequence 3039, Ap
741	4	8.2	339	5	US-09-833-245-2185	Sequence 2185, Ap	814	4	8.2	383	5	US-09-739-449-11796	Sequence 11796, A
742	4	8.2	339	5	US-09-833-245-2185	Sequence 2185, Ap	815	4	8.2	383	5	US-09-242-855A-2	Sequence 2, App1
743	4	8.2	340	5	US-09-739-449-10831	Sequence 10831, A	816	4	8.2	385	6	US-60-248-505-1167	Sequence 1167, Ap
744	4	8.2	340	5	US-09-821-803-2	Sequence 2, App1	817	4	8.2	386	1	PCT-US00-35017A-1306	Sequence 1306, Ap
745	4	8.2	340	5	US-09-417-540-20	Sequence 20, App1	818	4	8.2	387	5	US-09-826-509-436	Sequence 436, App
746	4	8.2	341	5	US-09-640-211A-1140	Sequence 1140, Ap	819	4	8.2	388	5	US-09-826-509-439	Sequence 439, App
747	4	8.2	341	6	US-60-248-505-938	Sequence 938, App	820	4	8.2	388	5	US-09-826-509-575	Sequence 575, App
748	4	8.2	342	1	PCT-US01-11988-1735	Sequence 1735, Ap	821	4	8.2	389	5	US-09-739-449-9550	Sequence 9550, Ap
749	4	8.2	342	1	US-09-833-245-1735	Sequence 1735, Ap	822	4	8.2	389	5	US-09-311-626B-18	Sequence 18, App1
750	4	8.2	344	1	PCT-US01-04098A-1568	Sequence 1568, Ap	823	4	8.2	390	1	PCT-US01-08117-32	Sequence 32, App1
751	4	8.2	344	5	US-09-739-449-11547	Sequence 11547, A	824	4	8.2	390	1	PCT-US01-04098A-3348	Sequence 3348, Ap
752	4	8.2	344	5	US-09-740-288A-8	Sequence 8, App1	825	4	8.2	390	5	US-09-739-449-12509	Sequence 12509, A
753	4	8.2	345	5	US-09-740-288A-20	Sequence 20, App1	826	4	8.2	392	1	PCT-US01-08975-16	Sequence 16, App1
754	4	8.2	345	5	US-09-379-095-12	Sequence 12, App1	827	4	8.2	392	1	PCT-US01-04098A-1754	Sequence 1754, Ap
755	4	8.2	345	1	US-09-708-489-11	Sequence 11, App1	828	4	8.2	392	1	PCT-US01-04098A-1788	Sequence 1788, Ap
756	4	8.2	346	1	PCT-US01-04098A-3010	Sequence 3010, Ap	829	4	8.2	394	5	US-09-813-718-16	Sequence 16, App1
757	4	8.2	346	5	US-09-343-011A-2	Sequence 2, App1	830	4	8.2	394	5	US-09-202-893B-2	Sequence 2, App1

831	4	8.2	396	5	US-09-640-211A-1055	Sequence 1055, Ap	904	4	8.2	449	5	US-09-739-449-12049	Sequence 12049, A
832	4	8.2	397	5	US-09-804-006-2	Sequence 2, Appl1	905	4	8.2	453	5	US-09-436-699A-16	Sequence 16, Ap
833	4	8.2	397	5	US-09-804-357-2	Sequence 2, Appl1	906	4	8.2	455	1	PCT-US01-11988-1147	Sequence 1147, Ap
834	4	8.2	397	5	US-09-717-778-2	Sequence 8296, Ap	907	4	8.2	455	1	PCT-US01-04098A-1845	Sequence 1845, Ap
835	4	8.2	398	5	US-09-739-449-8296	Sequence 527, App	908	4	8.2	455	1	US-09-833-245-1147	Sequence 1147, Ap
836	4	8.2	398	5	US-09-826-509-527	Sequence 86, Appl	909	4	8.2	456	5	PCT-US01-04098A-1368	Sequence 1368, Ap
837	4	8.2	399	4	US-08-861-774E-86	Sequence 9598, Ap	910	4	8.2	457	1	PCT-US00-35017A-1281	Sequence 1281, Ap
838	4	8.2	399	4	US-09-739-449-9598	Sequence 9713, Ap	911	4	8.2	458	1	PCT-US01-10484-67	Sequence 67, Ap
839	4	8.2	400	5	US-09-739-449-9713	Sequence 3, Appl1	912	4	8.2	458	1	PCT-US00-35017A-804	Sequence 804, Ap
840	4	8.2	400	5	US-09-769-970-3	Sequence 17, Appl	913	4	8.2	458	5	US-09-781-417-80	Sequence 80, Appl
841	4	8.2	400	5	US-09-769-970-17	Sequence 3456, Ap	914	4	8.2	458	5	US-09-436-699A-20	Sequence 20, Appl
842	4	8.2	401	1	PCT-US01-04098A-3456	Sequence 8777, Ap	915	4	8.2	458	5	US-09-827-040-9	Sequence 9, Appl1
843	4	8.2	401	1	US-09-739-449-8777	Sequence 13117, A	916	4	8.2	462	1	PCT-US01-04098A-1488	Sequence 1488, Ap
844	4	8.2	402	5	US-09-739-449-13117	Sequence 89, Appl	917	4	8.2	462	6	US-09-739-449-10681	Sequence 10681, A
845	4	8.2	402	6	US-60-248-823-89	Sequence 345, App	918	4	8.2	462	6	US-60-284-797-1	Sequence 1, Appl1
846	4	8.2	403	1	PCT-US01-11663-345	Sequence 574, App	919	4	8.2	463	1	PCT-US01-11988-212	Sequence 212, App
847	4	8.2	403	1	PCT-US01-11988-574	Sequence 574, App	920	4	8.2	463	5	US-09-833-245-212	Sequence 212, App
848	4	8.2	403	5	US-09-833-245-574	Sequence 574, App	921	4	8.2	463	6	US-60-284-797-3	Sequence 3, Appl1
849	4	8.2	405	5	US-09-833-245-574	Sequence 18, Appl	922	4	8.2	464	5	US-09-739-449-8859	Sequence 8859, Ap
850	4	8.2	406	1	PCT-US01-04098A-18	Sequence 1572, Ap	923	4	8.2	466	5	US-09-826-509-515	Sequence 515, App
851	4	8.2	407	5	US-09-739-449-8838	Sequence 8838, Ap	924	4	8.2	467	5	US-09-739-449-10221	Sequence 10221, A
852	4	8.2	407	5	US-09-784-208-4	Sequence 4, Appl1	925	4	8.2	468	1	PCT-US01-04098A-1834	Sequence 1834, Ap
853	4	8.2	409	1	PCT-US01-11988-1503	Sequence 1503, Ap	926	4	8.2	468	5	US-09-802-633-8	Sequence 8, Appl1
854	4	8.2	409	5	US-09-833-245-1503	Sequence 1503, Ap	927	4	8.2	468	5	US-09-832-129-59	Sequence 59, Appl
855	4	8.2	410	5	US-09-739-449-9844	Sequence 9844, Ap	928	4	8.2	470	6	US-60-248-505-706	Sequence 706, App
856	4	8.2	410	5	US-09-739-449-11188	Sequence 11188, A	929	4	8.2	472	5	US-09-739-449-10159	Sequence 10159, A
857	4	8.2	412	1	PCT-US01-11988-1676	Sequence 1676, Ap	930	4	8.2	472	5	US-09-603-1248-198	Sequence 198, App
858	4	8.2	412	5	US-09-833-245-1676	Sequence 1676, Ap	931	4	8.2	472	5	US-09-603-1248-200	Sequence 200, App
859	4	8.2	413	5	US-09-739-449-8208	Sequence 8208, Ap	932	4	8.2	475	1	PCT-US01-04098A-1290	Sequence 1290, Ap
860	4	8.2	413	5	US-09-739-449-10556	Sequence 10556, A	933	4	8.2	476	1	PCT-US01-04098A-3802	Sequence 3802, Ap
861	4	8.2	415	1	PCT-US01-08975-14	Sequence 14, Appl	934	4	8.2	476	5	US-09-423-844-164	Sequence 164, App
862	4	8.2	415	5	US-09-739-449-9402	Sequence 9402, Ap	935	4	8.2	476	5	US-09-433-510A-10	Sequence 10, Appl
863	4	8.2	415	5	US-09-739-449-11077	Sequence 11077, A	936	4	8.2	476	5	US-09-380-139A-164	Sequence 164, App
864	4	8.2	415	6	US-60-248-505-1149	Sequence 1149, Ap	937	4	8.2	477	1	PCT-US00-35017A-1325	Sequence 1325, Ap
865	4	8.2	416	1	PCT-US01-04098A-3756	Sequence 3756, Ap	938	4	8.2	478	1	PCT-US01-04098A-2998	Sequence 2998, Ap
866	4	8.2	417	5	US-09-739-449-9397	Sequence 9397, Ap	939	4	8.2	480	1	PCT-US01-11643-7	Sequence 7, Appl1
867	4	8.2	417	5	US-09-820-004-4	Sequence 4, Appl1	940	4	8.2	481	1	PCT-US01-04098A-3258	Sequence 3258, Ap
868	4	8.2	417	5	US-09-820-004-5	Sequence 5, Appl1	941	4	8.2	481	1	PCT-US00-35017A-1277	Sequence 1277, Ap
869	4	8.2	417	5	US-09-820-004-6	Sequence 6, Appl1	942	4	8.2	481	5	US-09-739-449-10445	Sequence 10445, A
870	4	8.2	417	5	US-09-308-823A-43	Sequence 43, Appl1	943	4	8.2	481	5	US-09-790-230-98	Sequence 98, Appl
871	4	8.2	418	5	US-09-739-449-10479	Sequence 10479, A	944	4	8.2	481	5	US-09-826-509-435	Sequence 435, App
872	4	8.2	419	1	PCT-US01-03401-14	Sequence 14, Appl	945	4	8.2	481	5	US-09-837-861-4	Sequence 4, Appl1
873	4	8.2	419	5	US-09-549-066-57	Sequence 57, Appl	946	4	8.2	482	5	US-09-826-509-165	Sequence 165, App
874	4	8.2	421	5	US-09-739-449-13306	Sequence 13306, A	947	4	8.2	483	1	PCT-US01-04098A-3257	Sequence 3257, Ap
875	4	8.2	422	6	US-60-248-505-1057	Sequence 1057, Ap	948	4	8.2	483	5	US-09-331-723A-14	Sequence 14, Appl
876	4	8.2	423	5	US-09-739-449-9353	Sequence 9353, Ap	949	4	8.2	484	1	PCT-US01-08975-10	Sequence 10, Appl
877	4	8.2	423	5	US-09-739-449-9353	Sequence 20, Appl1	950	4	8.2	484	1	PCT-US01-10484-45	Sequence 45, Appl
878	4	8.2	424	5	US-09-835-684-9	Sequence 9, Appl1	951	4	8.2	485	6	US-60-248-505-919	Sequence 919, Appl
879	4	8.2	424	5	US-09-739-449-11866	Sequence 11866, A	952	4	8.2	485	6	US-09-833-263-685	Sequence 685, App
880	4	8.2	429	1	PCT-US01-04098A-1407	Sequence 1407, Ap	953	4	8.2	486	5	PCT-US01-04098A-1026	Sequence 1026, Ap
881	4	8.2	430	1	US-08-956-171C-5244	Sequence 5244, Ap	954	4	8.2	488	1	US-09-806-080-2	Sequence 2, Appl1
882	4	8.2	430	5	US-09-739-449-9400	Sequence 9400, Ap	955	4	8.2	488	5	PCT-US01-11988-211	Sequence 211, App
883	4	8.2	430	5	US-09-739-449-9400	Sequence 10147, A	956	4	8.2	489	1	US-09-833-245-111	Sequence 111, App
884	4	8.2	431	5	PCT-US01-11988-2238	Sequence 2238, Ap	957	4	8.2	489	5	PCT-US01-01312-737	Sequence 737, App
885	4	8.2	432	1	PCT-US01-11988-2239	Sequence 2239, Ap	958	4	8.2	491	1	PCT-US01-01332-907	Sequence 907, App
886	4	8.2	432	1	PCT-US01-04098A-3536	Sequence 3536, Ap	959	4	8.2	492	5	US-09-739-449-12737	Sequence 12737, A
887	4	8.2	432	5	US-09-832-129-41	Sequence 41, Appl	960	4	8.2	492	5	US-09-723-630-4	Sequence 4, Appl1
888	4	8.2	432	5	US-09-832-129-54	Sequence 54, Appl	961	4	8.2	492	5	US-08-817-518-6	Sequence 6, Appl1
889	4	8.2	432	5	US-09-833-245-2238	Sequence 2238, Ap	962	4	8.2	496	4	US-09-819-386-4	Sequence 4, Appl1
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891	4	8.2	433	5	US-09-723-630-2	Sequence 2, Appl1	964	4	8.2	497	5	US-09-833-245-1593	Sequence 1593, Ap
892	4	8.2	434	5	US-09-723-630-2	Sequence 827, App	965	4	8.2	497	5	US-09-672-717-219	Sequence 219, App
893	4	8.2	435	5	US-09-549-066-53	Sequence 53, Appl	966	4	8.2	497	1	PCT-US01-11988-1593	Sequence 1593, Ap
894	4	8.2	437	1	PCT-US01-08975-12	Sequence 12, Appl	967	4	8.2	497	5	US-09-617-053A-4	Sequence 4, Appl1
895	4	8.2	437	1	PCT-US01-04098A-1380	Sequence 1380, Ap	968	4	8.2	497	5	US-09-833-245-1594	Sequence 1594, Ap
896	4	8.2	437	5	US-09-813-718-12	Sequence 12, Appl	969	4	8.2	497	5	US-09-672-717-219	Sequence 219, App
897	4	8.2	439	1	PCT-US01-11643-12	Sequence 12, Appl	970	4	8.2	498	1	PCT-US00-35017A-1063	Sequence 1063, App
898	4	8.2	441	5	US-09-549-066-44	Sequence 27, Appl	971	4	8.2	498	1	US-09-739-449-10057	Sequence 10057, A
899	4	8.2	444	1	PCT-US01-08117-27	Sequence 13, Appl	972	4	8.2	498	6	US-60-248-505-826	Sequence 826, App
900	4	8.2	444	1	US-09-403-269-13	Sequence 9229, Ap	973	4	8.2	500	1	PCT-US01-01332-1081	Sequence 1081, Ap
902	4	8.2	445	5	US-09-739-449-9229	Sequence 2, Appl1	975	4	8.2	500	1	US-60-248-505-1325	Sequence 1325, Ap
903	4	8.2	448	5	US-09-814-604-2		976	4	8.2	500	6		

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977 4 8.2 501 1 PCT-US01-04098A-1513 Sequence 1513, Ap
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979 4 8.2 503 5 US-09-739-449-11394 Sequence 11394, A
980 4 8.2 503 5 US-09-833-245-1883 Sequence 1883, A
981 4 8.2 503 6 US-09-820-765-889 Sequence 889, App
982 4 8.2 505 5 US-09-248-505-889 Sequence 2, Appl1
983 4 8.2 506 1 PCT-US01-04098A-3481 Sequence 3481, Ap
984 4 8.2 508 1 PCT-US01-04098A-3883 Sequence 3883, Ap
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986 4 8.2 511 1 PCT-US01-08117-89 Sequence 99, Appl1
987 4 8.2 512 1 PCT-US01-01312-654 Sequence 654, App
988 4 8.2 512 1 PCT-US01-01312-1080 Sequence 1080, Ap
989 4 8.2 514 5 US-09-739-449-12947 Sequence 12947, A
990 4 8.2 515 1 PCT-US01-04098A-2994 Sequence 2994, App
991 4 8.2 517 1 PCT-US01-01312-910 Sequence 910, App
992 4 8.2 518 1 PCT-US00-35017A-1453 Sequence 1453, Ap
993 4 8.2 519 5 US-09-817-183-2 Sequence 2, Appl1
994 4 8.2 519 6 US-60-248-505-1044 Sequence 1044, Ap
995 4 8.2 519 6 US-60-280-260-2 Sequence 2, Appl1
996 4 8.2 519 6 US-60-281-487-2 Sequence 1044, Ap
997 4 8.2 520 1 PCT-US01-04098A-1891 Sequence 1891, Ap
998 4 8.2 522 1 PCT-US01-01312-1138 Sequence 1138, Ap
999 4 8.2 524 1 PCT-US01-01312-761 Sequence 761, App
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## ALIGNMENTS

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RESULT 1
US-09-462-816-4
; Sequence 4, Application US/09462816
; GENERAL INFORMATION:
; APPLICANT: LI, Xiaomao
; APPLICANT: SAMBHARA, Suryaprakash
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES ENCODING G PROTEIN OF RESPIRATORY
; FILE REFERENCE: 1038-1003 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/462, 816
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: PCT/CA98/00697
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 08/896,442
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 232
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-462-816-4

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Best Local Similarity 100.0%; Pred. No. 8.6e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 10 KPNDHFHFVFNVPSCSNPTCAICKRIPNKKPGKK 49
DB 92 KPNDHFHFVFNVPSCSNPTCAICKRIPNKKPGKK 131

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RESULT 2
US-09-462-816-2
; Sequence 2, Application US/09462816
; GENERAL INFORMATION:
; APPLICANT: LI, Xiaomao
; APPLICANT: SAMBHARA, Suryaprakash
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES ENCODING G PROTEIN OF RESPIRATORY
; FILE REFERENCE: 1038-1003 MIS:jb

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; CURRENT APPLICATION NUMBER: US/09/462, 816
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: PCT/CA98/00697
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 08/896,442
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-09-462-816-2

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DB 158 KPNDHFHFVFNVPSCSNPTCAICKRIPNKKPGKK 197

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RESULT 3
US-09-739-449-9007
; Sequence 9007, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hunkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 9007
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9007

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Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 19 VFNFPV 24
DB 215 VFNFPV 220

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RESULT 4
US-09-739-449-8921
; Sequence 8921, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hunkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 8921
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-8921

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Best Local Similarity 100.0%; Pred. No. 9.5;  
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QY 19 VFNFPV 24  
DB 268 VFNFPV 273

RESULT 5  
US-09-654-289-9

; Sequence 9, Application US/09654289  
; GENERAL INFORMATION:  
; APPLICANT: Binz, Hans  
; APPLICANT: N'Guyen, Ngoc Thien  
; APPLICANT: Baussant, Thierry  
; APPLICANT: Trudel, Michel  
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY  
; TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Gordon W. Hueschen  
; STREET: 715 The "H" Bldg., 310 East Michigan  
; STREET: Avenue  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hueschen, Gordon W.  
; REGISTRATION NUMBER: 16,157  
; REFERENCE/DOCKET NUMBER: PF57PCTUS/d1n  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616-382-2030  
; TELEFAX: 616-382-2030  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 9  
; OTHER INFORMATION: /product="Orn"  
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US-09-654-289-9

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 SNNPT 33  
DB 4 SNNPT 8

RESULT 6  
US-09-654-289-11

; Sequence 11, Application US/09654289  
; GENERAL INFORMATION:  
; APPLICANT: Binz, Hans  
; APPLICANT: N'Guyen, Ngoc Thien  
; APPLICANT: Baussant, Thierry  
; APPLICANT: Trudel, Michel  
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY  
; TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL  
; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Gordon W. Hueschen  
; STREET: 715 The "H" Bldg., 310 East Michigan  
; STREET: Avenue  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hueschen, Gordon W.  
; REGISTRATION NUMBER: 16,157  
; REFERENCE/DOCKET NUMBER: PF57PCTUS/d1n  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 616-382-0030  
; TELEFAX: 616-382-2030  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
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; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 9  
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; OTHER INFORMATION: /note="sequence 174-187 / name : GI'adelac"  
US-09-654-289-11

Query Match 10.2%; Score 5; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 SNNPT 33  
DB 4 SNNPT 8

RESULT 7  
US-09-654-289-19

; Sequence 19, Application US/09654289  
; GENERAL INFORMATION:  
; APPLICANT: Binz, Hans  
; APPLICANT: N'Guyen, Ngoc Thien  
; APPLICANT: Baussant, Thierry  
; APPLICANT: Trudel, Michel  
; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY

;; TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL  
;; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS  
;; NUMBER OF SEQUENCES: 75  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Gordon W. Hueschen  
;; STREET: 715 The "H" Bldg., 310 East Michigan  
;; CITY: Kalamazoo  
;; STATE: MI  
;; COUNTRY: USA  
;; ZIP: 49007  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/654,289  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/721,979  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hueschen, Gordon W.  
;; REGISTRATION NUMBER: 16,157  
;; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 616-382-0030  
;; TELEFAX: 616-382-2030  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
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;; LOCATION: 12  
;; OTHER INFORMATION: /product="Orn"  
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QY 29 SNNPT 33  
DB 7 SNNPT 11  
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RESULT 8  
US-09-654-289-20  
;; Sequence 20, Application US/09654289  
;; GENERAL INFORMATION:  
;; APPLICANT: Binz, Hans  
;; APPLICANT: N'Guyen, Ngoc Thien  
;; APPLICANT: Baussant, Thierry  
;; APPLICANT: Trudel, Michel  
;; TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY  
;; TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL  
;; TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS  
;; NUMBER OF SEQUENCES: 75  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Gordon W. Hueschen

;; STREET: 715 The "H" Bldg., 310 East Michigan  
;; CITY: Kalamazoo  
;; STATE: MI  
;; COUNTRY: USA  
;; ZIP: 49007  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/654,289  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/721,979  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hueschen, Gordon W.  
;; REGISTRATION NUMBER: 16,157  
;; REFERENCE/DOCKET NUMBER: PF57PCTUS/dln  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 616-382-0030  
;; TELEFAX: 616-382-2030  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 12  
;; OTHER INFORMATION: /product="Orn"  
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;; OTHER INFORMATION: /note="sequence 171-187 / name : G4'AdeltaC"  
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;; US-09-654-289-20  
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 7 SNNPT 11  
;;  
RESULT 9  
US-09-722-329-107  
;; Sequence 107, Application US/09722329  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: 50 Human Secreted Proteins  
;; FILE REFERENCE: P2016P1  
;; CURRENT APPLICATION NUMBER: US/09/722,329  
;; CURRENT FILING DATE: 2000-11-28  
;; EARLIER APPLICATION NUMBER: 09/262,109  
;; EARLIER FILING DATE: 1999-03-04  
;; EARLIER APPLICATION NUMBER: 60/057,626  
;; EARLIER FILING DATE: 1997-09-05  
;; EARLIER APPLICATION NUMBER: 60/057,663  
;; EARLIER FILING DATE: 1997-09-05  
;; EARLIER APPLICATION NUMBER: 60/057,669  
;; EARLIER FILING DATE: 1997-09-05  
;; EARLIER APPLICATION NUMBER: 60/058,667  
;; EARLIER FILING DATE: 1997-09-12  
;; EARLIER APPLICATION NUMBER: 60/058,974  
;; EARLIER FILING DATE: 1997-09-12  
;; EARLIER APPLICATION NUMBER: 60/058,973  
;; EARLIER FILING DATE: 1997-09-12

EARLIER APPLICATION NUMBER: 60/058,666  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/090,112  
EARLIER FILING DATE: 1998-06-22  
NUMBER OF SEQ ID NOS: 206  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 107  
LENGTH: 26  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (26)  
OTHER INFORMATION: Xaa equals stop translation  
US-09-722-329-107

Query Match 10.2%; Score 5; DB 5; Length 26;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 26 SICSN 30  
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Db 21 SICSN 25\*

RESULT 10  
PCT-US00-01979A-264  
Sequence 264, Application PC/TUS0001979A  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognelix, Inc.  
TITLE OF INVENTION: Alpha-Conotoxin Peptides  
FILE REFERENCE: Alphas 2  
CURRENT APPLICATION NUMBER: PCT/US00/01979A  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/118,381  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 404  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 264  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Conus muscicus  
PCT-US00-01979A-264

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Best Local Similarity 100.0%; Pred. No. 18;  
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OY 30 NNPTC 34  
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Db 26 NNPTC 30

RESULT 11  
US-09-493-795A-264  
Sequence 264, Application US/09493795A  
GENERAL INFORMATION:  
APPLICANT: Watkins, Maren  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Hillyard, David R.  
APPLICANT: McIntosh, J. Michael  
TITLE OF INVENTION: Alpha-Conotoxin Peptides  
FILE REFERENCE: 2314-179.A  
CURRENT APPLICATION NUMBER: US/09/493,795A  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/118,381  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 404  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 264  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Conus muscicus  
US-09-493-795A-264

Query Match 10.2%; Score 5; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 NNPTC 34  
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Db 26 NNPTC 30

RESULT 12  
PCT-US01-01321-1293  
Sequence 1293, Application PC/TUS0101321  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc., et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC011PCT  
CURRENT APPLICATION NUMBER: PCT/US01/01321  
CURRENT FILING DATE: 2001-01-17  
NUMBER OF SEQ ID NOS: 2181  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1293  
LENGTH: 50  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (144)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (36)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
PCT-US01-01321-1293

Query Match 10.2%; Score 5; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORON 5  
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Db 39 KORON 43

RESULT 13  
PCT-US01-01339-3605  
Sequence 3605, Application PC/TUS0101339  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc., et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC006PCT  
CURRENT APPLICATION NUMBER: PCT/US01/01339  
CURRENT FILING DATE: 2001-03-17  
NUMBER OF SEQ ID NOS: 10231  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3605  
LENGTH: 52  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US01-01339-3605

Query Match 10.2%; Score 5; DB 1; Length 52;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPSKP 11

Db 37 PPSKP 41

Search completed: May 21, 2001, 14:18:57  
job time: 100 sec

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RESULT 14
PCT-US01-01321-1416
; Sequence 1416, Application PC/TUS0101321
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC011PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01321
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 2181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1416
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
PCT-US01-01321-1416

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Query Match          10.2%; Score 5; DB 1; Length 55;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QRONK 5

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RESULT 15
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; Sequence 3043, Application PC/TUS0101339
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01339
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3043
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
PCT-US01-01339-3043

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Query Match          10.2%; Score 5; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPSKP 11
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Db 22 PPSKP 26

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GenCore version 4.5  
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OM protein - protein search, using sw model

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149.546 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 49

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 390729 seqs, 57163235 residues

Word size : 0

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	49	100.0	49	19	W39217 Human RSV A subtyp
2	49	100.0	49	19	W39244 Human RSV G protei
3	49	100.0	49	19	W39248 Human RSV G protei
4	49	100.0	49	19	W39250 Human RSV G protei
5	49	100.0	49	19	W39251 Human RSV G protei
6	49	100.0	298	13	P70845 Sequence of human
7	49	100.0	298	13	R25302 HSRV glycoprotein
8	49	100.0	298	13	W47605 HSRV glycoprotein
9	49	100.0	681	10	P90441 Chimeric human res
10	48	98.0	49	19	W39219 Human RSV A subtyp
11	48	98.0	49	19	W39224 Human RSV A subtyp

12	46	93.9	49	19	W39220 Human RSV A subtyp
13	42	85.7	42	19	W39245 Human RSV G protei
14	40	81.6	43	20	W97304 Peptide which indu
15	40	81.6	49	19	W39218 Human RSV A subtyp
16	40	81.6	49	19	W39221 Human RSV A subtyp
17	40	81.6	49	19	W39222 Human RSV A subtyp
18	40	81.6	49	19	W39223 Human RSV A subtyp
19	40	81.6	59	17	R97073 Respiratory Syncyt
20	40	81.6	59	20	Y44100 RSV G protein anti
21	40	81.6	61	17	R97072 Respiratory Syncyt
22	40	81.6	61	20	Y44099 RSV G protein anti
23	40	81.6	101	16	R88253 RSV subgroup A wil
24	40	81.6	101	17	R95610 RSV sub-group A wi
25	40	81.6	101	17	R95616 Respiratory Syncyt
26	40	81.6	101	17	R97050 RSV G protein anti
27	40	81.6	101	20	Y44078 A G2Na peptide der
28	40	81.6	101	21	B18805 Secreted G protein
29	40	81.6	232	20	W96314 Respiratory syncit
30	40	81.6	298	14	R39286 Membrane bound G p
31	40	81.6	298	20	W96313 Streptococcal prot
32	40	81.6	349	17	R95660 Respiratory Syncyt
33	39	79.6	57	17	R97074 RSV G protein anti
34	39	79.6	57	20	Y44101 Respiratory Syncyt
35	37	75.5	55	17	R97075 RSV G protein anti
36	37	75.5	55	20	Y44102 Human RSV G protei
37	36	73.5	36	19	W39235 Human RSV G protei
38	36	73.5	36	19	W39236 Respiratory syncyt
39	36	73.5	37	17	R88817 Human RSV G protei
40	35	71.4	35	19	W39246 Human RSV G protei
41	35	71.4	35	19	W39249 Respiratory Syncyt
42	35	71.4	53	17	R97076 Respiratory Syncyt
43	35	71.4	53	20	Y44103 Peptide which indu
44	34	69.4	101	20	W97311 RSV G protein anti
45	33	67.3	33	17	R97078 Respiratory Syncyt
46	33	67.3	33	20	Y44105 RSV G protein anti
47	33	67.3	33	20	W97302 Peptide which indu
48	33	67.3	51	17	R97077 Respiratory Syncyt
49	33	67.3	51	20	Y44104 RSV G protein anti
50	33	67.3	101	20	W97310 Peptide which indu
51	32	65.3	32	17	R88813 Respiratory syncyt
52	29	59.2	29	19	W39247 Human RSV G protei
53	28	57.1	28	17	R88809 Respiratory syncyt
54	27	55.1	101	20	W97312 Peptide which indu
55	25	51.0	26	17	R87647 Synthetic RSV pept
56	22	44.9	23	17	R87648 Synthetic RSV pept
57	22	42.9	24	21	B15189 RSV G protein pept
58	21	42.9	24	21	Y95245 Respiratory syncyt
59	21	42.9	49	19	W39233 Human RSV G protei
60	19	38.8	19	19	W39237 Human RSV G protei
61	19	38.8	19	19	W39239 Human RSV G protei
62	19	38.8	19	19	W39240 Human RSV G protei
63	19	38.8	49	19	W39234 Human RSV G protei
64	17	34.7	17	17	R97064 Respiratory Syncyt
65	17	34.7	17	20	Y44091 RSV G protein anti
66	17	34.7	17	20	W93552 RSV attachment G p
67	17	34.7	17	20	W97315 Peptide which indu
68	16	32.7	16	20	W93549 RSV attachment G p
69	16	32.7	16	20	W93550 RSV attachment G p
70	15	30.6	15	19	W39238 Human RSV G protei
71	15	30.6	15	19	W39242 Human RSV G protei
72	15	30.6	15	19	W39243 Human RSV G protei
73	15	30.6	15	20	Y29703 Respiratory syncyt
74	15	30.6	15	20	W93553 RSV attachment G p
75	15	30.6	33	17	R97085 Respiratory Syncyt
76	15	30.6	33	20	Y44112 RSV G protein anti
77	15	30.6	51	17	R97084 Respiratory Syncyt
78	15	30.6	51	20	Y44111 RSV G protein anti
79	15	30.6	53	17	R97083 Respiratory Syncyt
80	15	30.6	53	20	Y44110 RSV G protein anti
81	15	30.6	55	17	R97082 Respiratory Syncyt
82	15	30.6	55	20	Y44109 RSV G protein anti
83	15	30.6	57	17	R97081 Respiratory Syncyt
84	15	30.6	57	20	Y44108 RSV G protein anti

85	15	30.6	59	17	R97080	Respiratory Syncyt	158	9	18.4	59	20	Y44121	RSV G protein anti
86	15	30.6	59	20	Y44107	Respiratory Syncyt	159	9	18.4	61	17	R97093	Respiratory Syncyt
87	15	30.6	61	17	R97079	Respiratory Syncyt	160	9	18.4	61	20	Y44120	RSV G protein anti
88	15	30.6	61	20	Y44106	RSV G protein anti	161	9	18.4	101	16	R88256	RSV subgroup B mod
89	15	30.6	101	16	R88235	RSV subgroup A mod	162	9	18.4	101	17	R95613	RSV subgp. B prote
90	15	30.6	101	17	R95612	RSV subgp. A prote	163	9	18.4	101	17	R95619	Respiratory Syncyt
91	15	30.6	101	17	R95618	RSV sub-group A mu	164	9	18.4	101	17	R97053	Respiratory Syncyt
92	15	30.6	101	17	R97052	Respiratory Syncyt	165	9	18.4	101	20	Y44081	RSV G protein anti
93	15	30.6	101	20	Y44080	RSV G protein anti	166	8	16.3	15	20	R97306	Peptide which indu
94	15	30.6	356	17	R95661	Immunogenic carrie	167	8	16.3	16	17	R97062	Respiratory Syncyt
95	14	28.6	14	16	R88245	Respiratory syncyt	168	8	16.3	16	20	R97300	Peptide which indu
96	14	28.6	14	17	R97054	Respiratory Syncyt	169	7	14.3	28	17	R95620	RSV sub-group B mu
97	14	28.6	14	20	Y44082	RSV G protein anti	170	7	14.3	244	13	R20929	Envelope proteins
98	14	28.6	14	20	W93551	RSV attachment G p	171	6	12.2	15	20	W93555	RSV attachment G p
99	14	28.6	15	20	W93554	Peptide which indu	172	6	12.2	17	17	R97066	Respiratory Syncyt
100	13	26.5	33	20	R97308	Peptide which indu	173	6	12.2	17	20	Y44093	RSV G protein anti
101	13	26.5	33	20	R88808	Respiratory syncyt	174	6	12.2	17	20	R97316	Peptide which indu
102	13	26.5	32	17	R88812	Respiratory syncyt	175	6	12.2	28	15	R65761	Peptide having int
103	13	26.5	33	17	R97092	Respiratory Syncyt	176	6	12.2	28	15	R65762	Human 28-mer pepti
104	13	26.5	33	20	Y44119	RSV G protein anti	177	6	12.2	75	21	B43901	Human cancer assoc
105	13	26.5	33	20	W97303	Peptide which indu	178	6	12.2	76	21	G57267	Arabidopsis thalia
106	13	26.5	37	17	R88816	Respiratory syncyt	179	6	12.2	128	21	G09850	Arabidopsis thalia
107	13	26.5	43	20	W97305	Peptide which indu	180	6	12.2	138	21	G09849	Arabidopsis thalia
108	13	26.5	49	19	W39225	Human RSV B subtyp	181	6	12.2	188	10	P93469	Sequence encoded b
109	13	26.5	49	19	W39226	Human RSV B subtyp	182	6	12.2	222	21	G36194	Arabidopsis thalia
110	13	26.5	49	19	W39227	Human RSV B subtyp	183	6	12.2	227	21	G14146	Arabidopsis thalia
111	13	26.5	49	19	W39228	Human RSV B subtyp	184	6	12.2	227	21	G43029	Arabidopsis thalia
112	13	26.5	49	19	W39229	Human RSV B subtyp	185	6	12.2	243	21	G14145	Arabidopsis thalia
113	13	26.5	49	19	W39230	Human RSV B subtyp	186	6	12.2	243	21	G43028	Arabidopsis thalia
114	13	26.5	49	19	W39231	Human RSV B subtyp	187	6	12.2	243	21	G51627	Arabidopsis thalia
115	13	26.5	51	17	R97091	Respiratory Syncyt	188	6	12.2	246	21	G14144	Arabidopsis thalia
116	13	26.5	51	20	Y44118	RSV G protein anti	189	6	12.2	246	21	G36193	Arabidopsis thalia
117	13	26.5	53	20	R97090	Respiratory Syncyt	190	6	12.2	246	21	G43027	Arabidopsis thalia
118	13	26.5	53	20	Y44117	RSV G protein anti	191	6	12.2	246	21	G51626	Arabidopsis thalia
119	13	26.5	55	17	R97089	Respiratory Syncyt	192	6	12.2	299	21	G51625	Arabidopsis thalia
120	13	26.5	55	20	Y44116	RSV G protein anti	193	6	12.2	337	20	Y00281	Human secreted pro
121	13	26.5	57	17	R97088	Respiratory Syncyt	194	6	12.2	359	21	G36192	Arabidopsis thalia
122	13	26.5	57	20	Y44115	RSV G protein anti	195	6	12.2	397	21	G31564	Arabidopsis thalia
123	13	26.5	59	17	R97087	Respiratory Syncyt	196	6	12.2	402	21	G31563	Arabidopsis thalia
124	13	26.5	59	20	Y44114	RSV G protein anti	197	6	12.2	402	21	G38778	Arabidopsis thalia
125	13	26.5	61	17	R97086	Respiratory Syncyt	198	6	12.2	409	8	P70284	Protein A - beta-g
126	13	26.5	61	20	Y44113	RSV G protein anti	199	6	12.2	411	21	G38777	Arabidopsis thalia
127	13	26.5	101	16	R88254	RSV subgroup B wi	200	6	12.2	412	20	Y59733	Human normal ovary
128	13	26.5	101	17	R95611	RSV subgp. B prote	201	6	12.2	415	21	G38776	Arabidopsis thalia
129	13	26.5	101	17	R95617	RSV sub-group B wi	202	6	12.2	416	21	G31562	Arabidopsis thalia
130	13	26.5	101	17	R97051	Respiratory Syncyt	203	6	12.2	421	8	P70283	Protein A - beta-g
131	13	26.5	101	20	Y44079	RSV G protein anti	204	6	12.2	483	5	P40694	Sequence encoded b
132	12	24.5	14	16	R88247	Respiratory Syncyt	205	6	12.2	483	5	P40181	Sequence encoded b
133	13	26.5	14	17	R97056	Respiratory Syncyt	206	6	12.2	508	13	R23850	Vasoactive intesti
134	12	24.5	14	20	Y44084	RSV G protein anti	207	6	12.2	516	5	P40135	Sequence of protei
135	12	24.5	14	20	Y01503	Peptide which indu	208	6	12.2	585	8	P70282	Protein A - beta-q
136	12	24.5	16	13	R28758	Glycoprotein G epi	209	6	12.2	1249	21	G50830	Arabidopsis thalia
137	12	24.5	17	17	R97065	Respiratory Syncyt	210	6	12.2	1254	21	G50829	Arabidopsis thalia
138	12	24.5	17	20	Y44092	RSV G protein anti	211	6	12.2	1268	21	G50828	Arabidopsis thalia
139	12	24.5	30	17	R95621	RSV sub-group A mu	212	5	10.2	9	16	R85720	Template peptide f
140	12	24.5	92	17	R95615	RSV subgp. A prote	213	5	10.2	11	21	B15365	Specific factor VI
141	12	24.5	101	17	R95614	RSV subgp. A prote	214	5	10.2	12	17	W05294	Template backbone
142	12	24.5	101	17	R97063	Respiratory Syncyt	215	5	10.2	13	19	W70131	Peptide produced b
143	12	24.5	101	20	Y44090	RSV G protein anti	216	5	10.2	14	16	R88249	Respiratory syncyt
144	10	20.4	10	19	W39241	Human RSV G protei	217	5	10.2	14	16	R88251	Respiratory Syncyt
145	10	20.4	15	20	W93548	Peptide which indu	218	5	10.2	14	17	R97058	Respiratory Syncyt
146	9	18.4	13	20	W97309	RSV attachment G p	219	5	10.2	14	17	R97060	Respiratory Syncyt
147	9	18.4	33	17	R97099	Peptide which indu	220	5	10.2	14	20	Y44086	RSV G protein anti
148	9	18.4	33	20	Y44126	RSV G protein anti	221	5	10.2	14	20	Y44088	RSV G protein anti
149	9	18.4	51	17	R97098	Respiratory Syncyt	222	5	10.2	14	20	W93567	RSV attachment G p
150	9	18.4	51	20	Y44125	Respiratory Syncyt	223	5	10.2	14	20	W97298	Peptide which indu
151	9	18.4	53	17	R97097	Respiratory Syncyt	224	5	10.2	15	19	W70149	Peptide produced b
152	9	18.4	53	20	Y44124	RSV G protein anti	225	5	10.2	17	17	R97068	Respiratory Syncyt
153	9	18.4	55	17	R97096	Respiratory Syncyt	226	5	10.2	17	17	R97069	Respiratory Syncyt
154	9	18.4	55	20	Y44123	RSV G protein anti	227	5	10.2	17	20	Y44095	Respiratory Syncyt
155	9	18.4	57	17	R97095	Respiratory Syncyt	228	5	10.2	17	20	Y44096	RSV G protein anti
156	9	18.4	57	20	Y44122	RSV G protein anti	229	5	10.2	18	14	R41939	Systemin. Lycoper
157	9	18.4	59	17	R97094	Respiratory Syncyt	230	5	10.2	18	20	W99102	Tomato systemin.

231	5	10.2	18	20	W97629	Tomato peptide hor	304	5	10.2	136	21	B54155	Human pancreatic c
232	5	10.2	18	21	B30686	Amino acid sequenc	305	5	10.2	138	21	B42439	Human ORFX ORF2203
233	5	10.2	19	18	W17416	Chicken anaemia vi	306	5	10.2	138	21	B08117	A polyphenol oxida
234	5	10.2	21	18	W14156	Human A33 antigen	307	5	10.2	139	18	W32903	Rat neurotrophic f
235	5	10.2	23	20	W86747	Anticoagulant pept	308	5	10.2	141	21	G27689	Arabidopsis thalia
236	5	10.2	23	20	W86748	Anticoagulant pept	309	5	10.2	141	21	G35313	Zea mays protein f
237	5	10.2	23	20	W86749	Anticoagulant pept	310	5	10.2	141	21	G57150	Arabidopsis thalia
238	5	10.2	23	20	W86745	Anticoagulant pept	311	5	10.2	142	21	B25507	Eucalyptus grandis
239	5	10.2	26	20	Y12955	Amino acid sequenc	312	5	10.2	143	21	G05220	Arabidopsis thalia
240	5	10.2	32	17	W02228	CD16:5:zeta(48-65)	313	5	10.2	143	21	G37407	Arabidopsis thalia
241	5	10.2	32	17	R89463	CD16:5:zeta(48-65)	314	5	10.2	145	18	W20455	H. pylori cytoplas
242	5	10.2	36	21	B21568	Cone snail alpha-c	315	5	10.2	145	18	W24664	H. pylori cytoplas
243	5	10.2	42	19	Y21513	Human neuroendocri	316	5	10.2	146	21	Y55838	Mouse SPOR01 poly
244	5	10.2	43	20	Y25813	Human secreted pro	317	5	10.2	147	20	Y29506	Human lung tumour
245	5	10.2	46	20	Y30875	Human secreted pro	318	5	10.2	147	21	B44445	Human lung tumour
246	5	10.2	47	21	B39022	Human secreted pro	319	5	10.2	148	21	G05046	Arabidopsis thalia
247	5	10.2	51	21	G09763	Arabidopsis thalia	320	5	10.2	148	21	G28877	Zea mays protein f
248	5	10.2	64	20	Y38401	Human secreted pro	321	5	10.2	152	21	G26876	Zea mays protein f
249	5	10.2	64	21	G33287	Zea mays protein f	322	5	10.2	152	21	B27614	Human secreted pro
250	5	10.2	67	21	B25316	Eucalyptus grandis	323	5	10.2	153	21	G12403	Zea mays protein f
251	5	10.2	68	21	B27618	Human secreted pro	324	5	10.2	154	21	G09456	Arabidopsis thalia
252	5	10.2	68	21	Y32145	Human secreted pro	325	5	10.2	154	21	Y81594	Streptococcus pneu
253	5	10.2	69	21	B12941	Neurotransmission	326	5	10.2	157	21	Y81594	Zea mays protein f
254	5	10.2	72	20	Y04915	Mycobacterium spec	327	5	10.2	158	21	G54449	Human lung tumour
255	5	10.2	73	21	Y69027	Amino acid sequenc	328	5	10.2	159	20	Y29505	Human lung tumour
256	5	10.2	77	18	W20189	H. pylori cytoplas	329	5	10.2	159	21	B44444	Zea mays protein f
257	5	10.2	79	21	G33475	Arabidopsis thalia	330	5	10.2	159	21	G40887	Human breast cance
258	5	10.2	84	22	B65013	Human secreted pro	331	5	10.2	161	18	W11587	Protein encoded by
259	5	10.2	86	13	R20695	Modified human pro	332	5	10.2	161	20	W88052	Fragment of gp30/a
260	5	10.2	86	13	R20693	Modified human pro	333	5	10.2	161	20	Y81899	Clone 2 of A. thal
261	5	10.2	86	13	R20694	Modified human pro	334	5	10.2	162	20	Y18128	Human FDF-beta3 cl
262	5	10.2	90	21	B25124	Eucalyptus grandis	335	5	10.2	163	16	R68567	Human FC99 phospho
263	5	10.2	93	21	B44361	Human secreted pro	336	5	10.2	164	18	W15254	Rat FC99 phosphory
264	5	10.2	96	16	R70799	Human secreted pro	337	5	10.2	164	18	W15258	Arabidopsis thalia
265	5	10.2	96	16	R70799	Human secreted pro	338	5	10.2	164	21	G27688	Zea mays protein f
266	5	10.2	98	21	B15805	Human chemokine I-	339	5	10.2	164	21	G54623	Arabidopsis thalia
267	5	10.2	99	21	G35451	Zea mays protein f	340	5	10.2	164	21	G57149	Arabidopsis thalia
268	5	10.2	99	21	G40827	Zea mays protein f	341	5	10.2	165	15	R51719	Partial sequence o
269	5	10.2	100	15	R51722	Partial sequence o	342	5	10.2	165	18	W32902	Rat neurotrophic f
270	5	10.2	100	21	B38309	Human secreted pro	343	5	10.2	165	21	G24740	Arabidopsis thalia
271	5	10.2	101	21	B53234	Human colon cancer	344	5	10.2	167	21	B53528	Human colon cancer
272	5	10.2	105	21	G56157	Arabidopsis thalia	345	5	10.2	168	21	G37406	Arabidopsis thalia
273	5	10.2	106	14	R41358	P. yoelii combined	346	5	10.2	168	21	G39345	Arabidopsis thalia
274	5	10.2	106	20	Y55723	FKHL17 forkhead dom	347	5	10.2	169	21	G54748	Arabidopsis thalia
275	5	10.2	106	20	Y55724	FKHL14 forkhead do	348	5	10.2	170	20	Y29215	Amino acid sequenc
276	5	10.2	107	21	G17879	Arabidopsis thalia	349	5	10.2	173	21	B25258	Eucalyptus grandis
277	5	10.2	107	21	G50035	Arabidopsis thalia	350	5	10.2	173	21	G36936	Arabidopsis thalia
278	5	10.2	107	21	G56156	Arabidopsis thalia	351	5	10.2	184	21	G05045	Arabidopsis thalia
279	5	10.2	108	21	G41963	Arabidopsis thalia	352	5	10.2	184	21	G08592	Arabidopsis thalia
280	5	10.2	109	15	R51721	Partial sequence o	353	5	10.2	184	21	G24739	Arabidopsis thalia
281	5	10.2	115	18	W28027	Amino acid sequenc	354	5	10.2	187	21	G40886	Zea mays protein f
282	5	10.2	115	21	G35314	Zea mays protein f	355	5	10.2	188	21	G08591	Arabidopsis thalia
283	5	10.2	116	21	G41962	Arabidopsis thalia	356	5	10.2	190	21	G29127	Arabidopsis thalia
284	5	10.2	120	21	B52089	Gene 38 human secr	357	5	10.2	190	21	G38040	Arabidopsis thalia
285	5	10.2	120	21	B52090	Human secreted pro	358	5	10.2	191	15	R54217	L.lactis branched
286	5	10.2	120	21	B21028	Human nucleic acid	359	5	10.2	191	15	R54217	L.lactis branched
287	5	10.2	120	21	G56155	Arabidopsis thalia	360	5	10.2	194	21	G23431	Arabidopsis thalia
288	5	10.2	121	16	R65201	VP3 protein, Chic	361	5	10.2	195	21	B42025	Human ORFX ORF1789
289	5	10.2	121	17	R88499	VP3 of chicken inf	362	5	10.2	195	21	B42025	Human ORFX ORF2360
290	5	10.2	121	18	W32904	Rat neurotrophic f	363	5	10.2	196	21	B42596	Arabidopsis thalia
291	5	10.2	122	17	B21854	Humanised light ch	364	5	10.2	197	21	G58186	Arabidopsis thalia
292	5	10.2	122	18	W21855	Humanised light ch	365	5	10.2	197	21	G58186	Arabidopsis thalia
293	5	10.2	122	18	W21855	Humanised light ch	366	5	10.2	200	14	R41938	Prosystemin, Lyco
294	5	10.2	127	18	W21855	Humanised light ch	367	5	10.2	200	20	W99101	Tomato prosystemin
295	5	10.2	127	18	W21855	Humanised light ch	368	5	10.2	200	20	W97625	Tomato prosystemin
296	5	10.2	128	21	B34068	Human secreted pro	369	5	10.2	200	20	W97625	Amino acid sequenc
297	5	10.2	130	21	B40509	Human ORFX ORF273	370	5	10.2	200	21	B30680	Cps9F protein whic
298	5	10.2	131	21	B58736	Breast and ovarian	371	5	10.2	200	21	Y68979	NK-lysin full len
299	5	10.2	131	21	G54450	Zea mays protein f	372	5	10.2	202	16	R77524	Arabidopsis thalia
300	5	10.2	132	21	B25142	Pinus radiata cell	373	5	10.2	203	21	G08590	Arabidopsis thalia
301	5	10.2	132	21	G27690	Arabidopsis thalia	374	5	10.2	203	21	G08590	F11 antigen protei
302	5	10.2	135	21	G54624	Zea mays protein f	375	5	10.2	205	20	W74465	Human prostate can
303	5	10.2	135	21	G57151	Arabidopsis thalia	376	5	10.2	205	21	B56481	Weissneria meningit

377	5	10.2	210	21	G45196	Arabidopsis thalia	450	5	10.2	273	20	Y08075	Human A33 protein
378	5	10.2	213	21	B19171	Amino acid sequenc	451	5	10.2	273	20	G23329	An A33 related ant
379	5	10.2	214	19	B95808	S. pneumoniae deri	452	5	10.2	273	21	G08347	Arabidopsis thalia
380	5	10.2	217	20	W88104	A Rab protein desi	453	5	10.2	273	21	G32582	Arabidopsis thalia
381	5	10.2	217	21	G24738	Arabidopsis thalia	454	5	10.2	273	21	G51392	Arabidopsis thalia
382	5	10.2	219	21	G16787	Arabidopsis thalia	455	5	10.2	274	21	G13887	Arabidopsis thalia
383	5	10.2	219	21	G76981	Quail H1 histone p	456	5	10.2	274	21	G20760	Arabidopsis thalia
384	5	10.2	220	14	R39700	Peptide sequence h	457	5	10.2	274	21	G39344	Arabidopsis thalia
385	5	10.2	220	16	R80553	S-SPV-001 potentia	458	5	10.2	274	21	G45184	Arabidopsis thalia
386	5	10.2	220	19	Y11027	H. pylori ORF 02ge	459	5	10.2	274	21	G45195	Arabidopsis thalia
387	5	10.2	220	20	Y17195	H. pylori outer me	460	5	10.2	275	21	G09455	Arabidopsis thalia
388	5	10.2	221	19	W80645	S. pneumoniae prot	461	5	10.2	276	20	Y34505	Porphyromonas ging
389	5	10.2	221	21	G05416	Arabidopsis thalia	462	5	10.2	280	20	Y34378	Porphyromonas ging
390	5	10.2	221	21	Y74740	Neisseria gonorrhe	463	5	10.2	280	21	B39283	Gene 15 human secr
391	5	10.2	224	12	R11494	Endothelin-3 precu	464	5	10.2	284	21	G39783	Arabidopsis thalia
392	5	10.2	224	13	R25159	Endothelin-3 precu	465	5	10.2	285	21	G04683	Arabidopsis thalia
393	5	10.2	225	21	G31905	Arabidopsis thalia	466	5	10.2	285	21	G21575	Arabidopsis thalia
394	5	10.2	225	21	G05445	Arabidopsis thalia	467	5	10.2	285	21	G53563	Arabidopsis thalia
395	5	10.2	226	14	R38875	Sequence of haemag	468	5	10.2	286	17	W03566	Mycobacterium tube
396	5	10.2	226	15	R60213	Immunogenic fragme	469	5	10.2	286	20	Y19836	B. burgdorferi ant
397	5	10.2	226	17	W09318	Human wild type ch	470	5	10.2	290	21	B54365	Human pancreatic c
398	5	10.2	226	17	W09319	Human chymase clon	471	5	10.2	290	21	G21313	Arabidopsis thalia
399	5	10.2	226	17	W09320	Human chymase clon	472	5	10.2	291	21	G54148	Arabidopsis thalia
400	5	10.2	226	19	Y85978	S. pneumoniae deri	473	5	10.2	292	21	G04662	Arabidopsis thalia
401	5	10.2	228	21	G58185	Arabidopsis thalia	474	5	10.2	292	21	G53562	Arabidopsis thalia
402	5	10.2	229	17	R95274	Nisin nlsR gene pr	475	5	10.2	298	16	R68575	Arabidopsis thalia
403	5	10.2	229	21	G17425	Arabidopsis thalia	476	5	10.2	298	19	W61379	Rat NDF encoded by
404	5	10.2	230	21	G11474	Arabidopsis thalia	477	5	10.2	299	20	Y08071	Human junctional a
405	5	10.2	231	16	R68570	Rat NDF encoded by	478	5	10.2	299	20	Y23321	Human PRO307 prote
406	5	10.2	231	22	B36603	Human FLEXHR-25 pr	479	5	10.2	299	20	Y13364	Amino acid sequenc
407	5	10.2	233	21	G11473	Arabidopsis thalia	480	5	10.2	299	20	W74465	Amino acid sequenc
408	5	10.2	236	20	Y09153	Human CD81m protei	481	5	10.2	299	21	B24405	F11 antigen protei
409	5	10.2	238	13	R23785	Prepro ET-3 sequen	482	5	10.2	299	21	G36935	Human PRO301 prote
410	5	10.2	239	21	B43632	Human cancer assoc	483	5	10.2	299	21	Y95344	Arabidopsis thalia
411	5	10.2	239	21	G07529	Arabidopsis thalia	484	5	10.2	299	21	Y70670	Human PRO301 prote
412	5	10.2	239	21	G11472	Arabidopsis thalia	485	5	10.2	299	21	Y76011	Human A33 receptor
413	5	10.2	240	13	R20928	Envelope proteins	486	5	10.2	299	21	Y76011	Human A33 receptor
414	5	10.2	241	13	R29574	Human heregulin-be	487	5	10.2	299	22	B55950	Skin cell protein,
415	5	10.2	241	17	R87468	Glial growth facto	488	5	10.2	299	22	B56015	Human angioogenesis
416	5	10.2	241	20	Y06637	Herugelin-beta-3.	489	5	10.2	299	22	B53086	Mouse homo sapien
417	5	10.2	241	21	Y71174	Human Heregulin HR	490	5	10.2	300	15	G6481	Mouse functional a
418	5	10.2	242	21	G17424	Arabidopsis thalia	491	5	10.2	300	19	W61380	Amino acid sequenc
419	5	10.2	245	21	G36996	Arabidopsis thalia	492	5	10.2	300	19	W37928	A33 related antige
420	5	10.2	245	21	G53882	Arabidopsis thalia	493	5	10.2	300	20	Y23325	Arabidopsis thalia
421	5	10.2	246	18	W20840	H. pylori cytoplas	494	5	10.2	300	21	G16786	Arabidopsis thalia
422	5	10.2	246	21	B58196	Lung cancer associ	495	5	10.2	305	21	Y97042	B. subtilis oppc m
423	5	10.2	247	20	W73878	Human chymase prot	496	5	10.2	305	21	G04661	Arabidopsis thalia
424	5	10.2	247	21	B42519	Human OREP ORF2283	497	5	10.2	305	21	G53561	Arabidopsis thalia
425	5	10.2	248	17	R88712	Tunicate serine pr	498	5	10.2	306	21	G16785	Arabidopsis thalia
426	5	10.2	248	20	Y39924	Bovine rotavirus W	499	5	10.2	317	20	Y19969	B. burgdorferi ant
427	5	10.2	248	21	Y77988	Human MBP amino ac	500	5	10.2	317	21	G37740	Arabidopsis thalia
428	5	10.2	251	19	W53008	Mus musculus I-mfb	501	5	10.2	318	18	W14158	Mouse A33 antigen.
429	5	10.2	255	21	C58184	Arabidopsis thalia	502	5	10.2	318	20	Y74150	Human prostate tum
430	5	10.2	257	21	G07568	Arabidopsis thalia	503	5	10.2	318	21	G07743	Arabidopsis thalia
431	5	10.2	257	21	G17567	Arabidopsis thalia	504	5	10.2	318	21	G08190	Arabidopsis thalia
432	5	10.2	257	21	G52536	Arabidopsis thalia	505	5	10.2	319	18	W14146	Human A33 antigen.
433	5	10.2	258	21	G21577	Arabidopsis thalia	506	5	10.2	319	20	Y23323	Amino acid sequenc
434	5	10.2	258	21	G39785	Arabidopsis thalia	507	5	10.2	319	22	B65863	Human A33 protein
435	5	10.2	259	21	G36995	Arabidopsis thalia	508	5	10.2	320	22	B60094	Human transport pr
436	5	10.2	259	21	G53881	Arabidopsis thalia	509	5	10.2	323	21	G36934	Arabidopsis thalia
437	5	10.2	260	20	Y08072	Human DNA40628 pro	510	5	10.2	324	17	R88558	V.harveyi lucifera
438	5	10.2	260	20	Y23326	An A33 related ant	511	5	10.2	325	17	W03565	Mycobacterium tube
439	5	10.2	261	12	R13505	P.denitrificans CO	512	5	10.2	325	21	B51703	Gene 34 human secr
440	5	10.2	262	21	G37741	Arabidopsis thalia	513	5	10.2	325	21	Y97281	Fibronectin attach
441	5	10.2	262	21	G45775	Arabidopsis thalia	514	5	10.2	326	21	G06827	Arabidopsis thalia
442	5	10.2	263	20	Y08074	Human DNA40628 pro	515	5	10.2	326	21	G49383	Arabidopsis thalia
443	5	10.2	263	20	Y23328	An A33 related ant	516	5	10.2	327	21	Y74737	Neisseria gonorrhe
444	5	10.2	268	20	Y08073	Human A33 protein.	517	5	10.2	327	21	B39359	Human secreted pro
445	5	10.2	270	20	Y23327	An A33 related ant	518	5	10.2	328	21	G54896	Arabidopsis thalia
446	5	10.2	270	20	Y19837	B. burgdorferi ant	519	5	10.2	329	21	G39343	Arabidopsis thalia
447	5	10.2	270	21	G21576	Arabidopsis thalia	520	5	10.2	330	16	R79967	Fifth transmembran
448	5	10.2	270	21	G39784	Arabidopsis thalia	521	5	10.2	332	18	W32418	Mycobacterium tube
449	5	10.2	272	21	B54235	Human pancreatic c	522	5	10.2	332	18	W32350	Mycobacterium tube

523	5	10.2	332	19	W81683	M. tuberculosis im	596	404	21	G45866	Arabidopsis thalia
524	5	10.2	332	19	W64322	Mycobacterium tube	597	406	20	Y49152	Amino acid sequenc
525	5	10.2	332	20	Y39083	M. tuberculosis an	598	409	21	G59031	Arabidopsis thalia
526	5	10.2	332	20	Y38945	M. tuberculosis re	599	410	19	W77354	Human telomere rep
527	5	10.2	332	21	G36394	Arabidopsis thalia	600	412	20	Y49151	Amino acid sequenc
528	5	10.2	332	21	G37924	Arabidopsis thalia	601	413	18	W20789	H. pylori cytoplas
529	5	10.2	332	21	Y74739	Neisseria meningit	602	414	21	G30649	Arabidopsis thalia
530	5	10.2	336	20	Y19968	B. burgdorferi ant	603	416	21	G43150	Arabidopsis thalia
531	5	10.2	337	21	G41778	Arabidopsis thalia	604	418	20	Y37459	Protein involved i
532	5	10.2	337	21	G52535	Arabidopsis thalia	605	418	21	G59030	Arabidopsis thalia
533	5	10.2	343	12	R13276	Tobacco extracellu	606	419	18	W20872	H. pylori secreted
534	5	10.2	343	18	W31298	Nicotiana sp. extr	607	419	20	Y42443	N-terminal region
535	5	10.2	343	21	B07514	Amino acid sequenc	608	419	20	Y32182	N-terminal choline
536	5	10.2	343	21	G52534	Arabidopsis thalia	609	419	20	Y49149	Amino acid sequenc
537	5	10.2	343	21	Y44577	Xylitol dehydrogen	610	419	21	G18199	Arabidopsis thalia
538	5	10.2	344	21	G06611	Human porphobilino	611	419	21	G27322	Arabidopsis thalia
539	5	10.2	344	21	G27323	Arabidopsis thalia	612	419	21	G50028	Human heregulin-be
540	5	10.2	348	20	Y25806	Human secreted pro	613	420	13	R29575	Herugelin-beta-2-1
541	5	10.2	350	21	G07251	Arabidopsis thalia	614	420	20	Y06638	Human Heregulin HR
542	5	10.2	350	21	G43383	Arabidopsis thalia	615	420	21	Y71175	Parasporium rhizob
543	5	10.2	354	21	G13829	Arabidopsis thalia	616	422	6	P50775	Rat NR5F. Rattus
544	5	10.2	354	21	G29125	Arabidopsis thalia	617	422	14	R43651	Human NR5F. Homo
545	5	10.2	361	20	Y30874	Human secreted pro	618	422	14	R51269	GGR-II encoded by
546	5	10.2	364	21	G51816	Arabidopsis thalia	619	422	15	R55854	GGR-II encoded by
547	5	10.2	364	21	G52519	Arabidopsis thalia	620	422	15	R46923	Rat NDF encoded by
548	5	10.2	366	21	G08189	Arabidopsis thalia	621	422	16	R68569	Rat NDF. Rattus r
549	5	10.2	366	21	G43152	Arabidopsis thalia	622	422	16	R68568	Human glial cell g
550	5	10.2	368	21	G07250	Arabidopsis thalia	623	422	16	R67258	Human neuregulin G
551	5	10.2	368	21	G43382	Arabidopsis thalia	624	422	17	W09371	Human GGF2. Homo
552	5	10.2	369	21	G20759	Arabidopsis thalia	625	422	17	W09372	Glial growth facto
553	5	10.2	372	22	B28788	Protein encoded by	626	422	17	R96081	Glial growth facto
554	5	10.2	373	21	Y99446	Human PRO1781 (UNQ	627	422	17	R87466	Glial growth facto
555	5	10.2	374	21	G06826	Arabidopsis thalia	628	422	17	R87467	Glial growth facto
556	5	10.2	374	21	G49382	Arabidopsis thalia	629	422	17	R86628	Mature hGF2. Hom
557	5	10.2	376	20	Y37222	Protein which is s	630	425	20	Y49248	N-terminal region
558	5	10.2	377	21	G45774	Arabidopsis thalia	631	425	20	Y32187	N-terminal choline
559	5	10.2	378	17	R99796	Biotin synthetic e	632	425	21	G41889	Arabidopsis thalia
560	5	10.2	378	20	W73908	A. thaliana biotin	633	426	21	G41777	Arabidopsis thalia
561	5	10.2	378	21	G45773	Arabidopsis thalia	634	429	22	B36588	Human FLEXHM-10 pr
562	5	10.2	379	21	Y15155	Human prostate ser	635	430	21	G21312	Arabidopsis thalia
563	5	10.2	383	21	G20551	Arabidopsis thalia	636	430	21	G51814	Arabidopsis thalia
564	5	10.2	383	21	G50026	Arabidopsis thalia	637	430	21	G54147	Arabidopsis thalia
565	5	10.2	384	21	G08346	Arabidopsis thalia	638	432	20	Y32445	N-terminal region
566	5	10.2	384	21	G32581	Arabidopsis thalia	639	433	20	Y32184	N-terminal choline
567	5	10.2	384	21	G51391	Arabidopsis thalia	640	433	21	G48155	Arabidopsis thalia
568	5	10.2	385	21	G08345	Arabidopsis thalia	641	434	20	Y13567	Human Robo 2 polyp
569	5	10.2	385	21	G32580	Arabidopsis thalia	642	434	20	Y08405	Human partial ROBO
570	5	10.2	385	21	G51390	Arabidopsis thalia	643	436	15	R56658	Aminopeptidase pep
571	5	10.2	391	21	Y34946	Chlamydia pneumoni	644	436	19	Y11029	H. pylori ORF 01cp
572	5	10.2	391	21	G18198	Arabidopsis thalia	645	451	14	R31184	GABA-A receptor al
573	5	10.2	391	21	G45868	Arabidopsis thalia	646	451	15	R59862	Human GABA recepto
574	5	10.2	392	21	G18197	Arabidopsis thalia	647	451	18	W16328	Human host cell pr
575	5	10.2	392	21	G45867	Arabidopsis thalia	648	453	21	G21311	Arabidopsis thalia
576	5	10.2	393	21	G35663	Arabidopsis thalia	649	453	21	G54146	Arabidopsis thalia
577	5	10.2	393	21	G51815	Arabidopsis thalia	650	455	15	R57771	Mouse nucleobindin
578	5	10.2	393	21	G52518	Arabidopsis thalia	651	456	19	W77355	Altered telomere r
579	5	10.2	394	21	G05314	Arabidopsis thalia	652	456	19	W48628	Rat liver ribonucle
580	5	10.2	394	21	G39979	Arabidopsis thalia	653	456	21	G41776	Arabidopsis thalia
581	5	10.2	395	21	G13828	Arabidopsis thalia	654	457	21	G10061	Arabidopsis thalia
582	5	10.2	396	21	B26416	Drosophila melanog	655	461	16	R68572	Rat NDF encoded by
583	5	10.2	396	21	B20920	Drosophila odorant	656	461	16	R68571	Rat NDF encoded by
584	5	10.2	398	21	G29696	Arabidopsis thalia	657	461	21	G25647	Arabidopsis thalia
585	5	10.2	400	18	W20375	H. pylori secreted	658	462	16	R68562	Human NDF-alpha2b
586	5	10.2	400	21	G20550	Arabidopsis thalia	659	462	16	R68561	Human prNDP-alpha
587	5	10.2	400	21	G50025	Arabidopsis thalia	660	463	21	B16688	Bacteriophage bp-1
588	5	10.2	402	21	G08188	Arabidopsis thalia	661	463	21	G30392	Arabidopsis thalia
589	5	10.2	402	21	G39978	Arabidopsis thalia	662	465	21	B57042	Human prostate can
590	5	10.2	402	21	G43151	Arabidopsis thalia	663	468	21	G10060	Arabidopsis thalia
591	5	10.2	403	21	G05313	Arabidopsis thalia	664	473	21	B42243	Human ORFX ORF2007
592	5	10.2	403	21	G18200	Arabidopsis thalia	665	474	14	R31582	Sequence encoded b
593	5	10.2	403	21	G50029	Arabidopsis thalia	666	474	18	W39084	Human ShcC mutant
594	5	10.2	404	21	G13827	Arabidopsis thalia	667	474	18	W39085	Human ShcC mutant
595	5	10.2	404	21	G18196	Arabidopsis thalia	668	474	18	W39086	Human ShcC mutant

669	5	10.2	474	18	W39088	Human ShcC mutant	742	5	10.2	578	19	W40042	Biologically equiv
670	5	10.2	474	18	W39089	Human ShcC mutant	743	5	10.2	578	19	W40043	Biologically equiv
671	5	10.2	474	18	W39090	Human ShcC mutant	744	5	10.2	578	19	W40044	Biologically equiv
672	5	10.2	474	18	W39091	Human ShcC mutant	745	5	10.2	578	19	W40045	Biologically equiv
673	5	10.2	474	18	W39092	Human ShcC mutant	746	5	10.2	581	20	Y42774	Rat neuronal immed
674	5	10.2	474	18	W39093	Human ShcC mutant	747	5	10.2	584	20	Y15222	Human receptor pro
675	5	10.2	474	18	W39094	Human ShcC mutant	748	5	10.2	586	11	R07998	Asparagine synthet
676	5	10.2	474	18	W39096	Human ShcC mutant	749	5	10.2	586	21	B27304	A. thaliana NIM1 h
677	5	10.2	474	18	W23246	Human ShcC protein	750	5	10.2	586	21	G41887	Arabidopsis thalia
678	5	10.2	474	18	W39087	Human ShcC mutant	751	5	10.2	587	21	G52977	Arabidopsis thalia
679	5	10.2	474	18	W15253	Human brain-specific	752	5	10.2	588	21	G49517	Arabidopsis thalia
680	5	10.2	474	18	W15257	Rat brain-specific	753	5	10.2	591	18	W37399	Human sex comb on
681	5	10.2	476	18	W24089	Balanus amphitrite	754	5	10.2	591	18	W37395	Human sex comb on
682	5	10.2	479	21	G25646	Arabidopsis thalia	755	5	10.2	591	20	Y18289	Human Scm protein
683	5	10.2	479	21	G41888	Arabidopsis thalia	756	5	10.2	593	19	W98782	H. pylori GHPO 120
684	5	10.2	482	21	B18316	Plasmodium falcipa	757	5	10.2	594	18	W15260	Rat brain-specific
685	5	10.2	485	21	B10906	S. aureus D1TA pro	758	5	10.2	594	18	W15256	Human brain-specif
686	5	10.2	487	16	R79965	Human histamine H1	759	5	10.2	595	16	R81314	Yeast TIHL. Sacch
687	5	10.2	487	16	R71909	Human histamine H1	760	5	10.2	595	19	W54167	S. cerevisiae TIH1
688	5	10.2	488	21	R83288	Borrelia antigenic	761	5	10.2	595	20	W87487	S. cerevisiae TIH1
689	5	10.2	491	14	R36979	Histamine H1 recep	762	5	10.2	603	19	W40040	A Haemophilus infl
690	5	10.2	491	15	R48059	Sequence of protea	763	5	10.2	615	16	R74630	Tomato TGTR1 ethy
691	5	10.2	496	21	B25531	Eucalyptus grandis	764	5	10.2	615	19	W73126	Tomato ethylene re
692	5	10.2	498	15	R55800	Interleukin 14. H	765	5	10.2	619	16	R77545	MEKK2 protein. Mu
693	5	10.2	499	20	W30848	A. thaliana xylan	766	5	10.2	619	19	W56158	A mitogen-activate
694	5	10.2	500	19	W77356	Human telomere rep	767	5	10.2	619	20	Y43319	Mitogen ERK kinase
695	5	10.2	500	20	Y02185	A human telomere r	768	5	10.2	619	20	Y42108	Murine MEKK2 prote
696	5	10.2	501	20	Y17293	Mouse cell death p	769	5	10.2	619	20	W73532	MEKK2 protein. Ma
697	5	10.2	501	20	Y01097	PREACL1 protein.	770	5	10.2	619	21	R01217	Murine MEKK2. Mus
698	5	10.2	501	21	G53411	Arabidopsis thalia	771	5	10.2	620	18	W37397	Human sex comb on
699	5	10.2	501	21	Y54311	Amino acid sequenc	772	5	10.2	620	18	W37393	Human sex comb on
700	5	10.2	502	20	Y17292	Human cell death p	773	5	10.2	620	20	Y18287	Human Scm protein
701	5	10.2	503	21	G35662	Arabidopsis thalia	774	5	10.2	620	21	G32089	Arabidopsis thalia
702	5	10.2	503	21	G52517	Arabidopsis thalia	775	5	10.2	622			

815	5	10.2	675	19	W74488	Amino acid sequenc	888	5	10.2	683	17	W17645	Thermoanaerobacter
816	5	10.2	675	19	W74486	Amino acid sequenc	889	5	10.2	683	17	W17646	CGTase variant 146
817	5	10.2	675	19	W74485	Degenerate amino a	890	5	10.2	683	17	W17647	CGTase variant 145
818	5	10.2	675	19	W74504	Amino acid sequenc	891	5	10.2	683	17	W17648	CGTase variant 145
819	5	10.2	675	19	W74503	Amino acid sequenc	892	5	10.2	683	17	W17651	Thermoanaerobacter
820	5	10.2	675	19	W74502	Amino acid sequenc	893	5	10.2	683	17	W17622	Thermoanaerobacter
821	5	10.2	675	19	W74501	Amino acid sequenc	894	5	10.2	683	17	W17623	Thermoanaerobacter
822	5	10.2	675	19	W74500	Amino acid sequenc	895	5	10.2	683	17	W17624	Thermoanaerobacter
823	5	10.2	675	19	W74499	Amino acid sequenc	896	5	10.2	683	17	W17625	Thermoanaerobacter
824	5	10.2	675	19	W74498	Amino acid sequenc	897	5	10.2	683	17	W17626	Thermoanaerobacter
825	5	10.2	675	19	W74497	Amino acid sequenc	898	5	10.2	683	17	W17627	Thermoanaerobacter
826	5	10.2	675	19	W74496	Amino acid sequenc	899	5	10.2	683	17	W17628	Thermoanaerobacter
827	5	10.2	675	19	W74495	Amino acid sequenc	900	5	10.2	683	17	W17629	Thermoanaerobacter
828	5	10.2	675	19	W74494	Amino acid sequenc	901	5	10.2	683	17	W17630	Thermoanaerobacter
829	5	10.2	675	19	W74493	Amino acid sequenc	902	5	10.2	683	17	W17631	Thermoanaerobacter
830	5	10.2	675	19	W74492	Amino acid sequenc	903	5	10.2	683	17	W17632	Thermoanaerobacter
831	5	10.2	675	19	W74491	Amino acid sequenc	904	5	10.2	683	17	W17633	Thermoanaerobacter
832	5	10.2	675	19	W74490	Amino acid sequenc	905	5	10.2	683	17	W17610	Thermoanaerobacter
833	5	10.2	675	19	W74489	Amino acid sequenc	906	5	10.2	683	17	W17613	Thermoanaerobacter
834	5	10.2	675	19	W74509	Amino acid sequenc	907	5	10.2	683	17	W17614	Thermoanaerobacter
835	5	10.2	675	19	W74508	Amino acid sequenc	908	5	10.2	683	17	W17616	Thermoanaerobacter
836	5	10.2	675	19	W74507	Amino acid sequenc	909	5	10.2	683	17	W17617	Thermoanaerobacter
837	5	10.2	675	19	W74506	Amino acid sequenc	910	5	10.2	683	17	W17634	Thermoanaerobacter
838	5	10.2	675	19	W74505	Amino acid sequenc	911	5	10.2	683	17	W17635	Thermoanaerobacter
839	5	10.2	675	21	W71172	Human Heregulin HR	912	5	10.2	683	17	W17636	Thermoanaerobacter
840	5	10.2	675	21	W71178	Human Heregulin HR	913	5	10.2	683	17	W17618	Thermoanaerobacter
841	5	10.2	675	21	W71179	Human Heregulin HR	914	5	10.2	683	17	W17619	Thermoanaerobacter
842	5	10.2	675	21	W71180	Human Heregulin HR	915	5	10.2	683	17	W17620	Thermoanaerobacter
843	5	10.2	675	21	W71181	Human Heregulin HR	916	5	10.2	684	17	W17621	Thermoanaerobacter
844	5	10.2	675	21	W71182	Human Heregulin HR	917	5	10.2	684	17	W17580	Thermoanaerobacter
845	5	10.2	675	21	W71183	Human Heregulin HR	918	5	10.2	684	17	W17581	Thermoanaerobacter
846	5	10.2	675	21	W71184	Human Heregulin HR	919	5	10.2	684	17	W17583	Thermoanaerobacter
847	5	10.2	675	21	W71185	Human Heregulin HR	920	5	10.2	684	17	W17584	Thermoanaerobacter
848	5	10.2	675	21	W71186	Human Heregulin HR	921	5	10.2	684	17	W17585	Thermoanaerobacter
849	5	10.2	675	21	W71187	Human Heregulin HR	922	5	10.2	684	17	W17587	Thermoanaerobacter
850	5	10.2	675	21	W71188	Human Heregulin HR	923	5	10.2	684	17	W17588	Thermoanaerobacter
851	5	10.2	675	21	W71189	Human Heregulin HR	924	5	10.2	684	17	W17589	Thermoanaerobacter
852	5	10.2	675	21	W71190	Human Heregulin HR	925	5	10.2	684	17	W17591	Thermoanaerobacter
853	5	10.2	675	21	W71191	Human Heregulin HR	926	5	10.2	685	17	W17582	Thermoanaerobacter
854	5	10.2	675	21	W71192	Human Heregulin HR	927	5	10.2	685	17	W17586	Thermoanaerobacter
855	5	10.2	675	21	W71193	Human Heregulin HR	928	5	10.2	685	17	W17590	Thermoanaerobacter
856	5	10.2	675	21	W71194	Human Heregulin HR	929	5	10.2	685	21	G51803	Arabidopsis thalia
857	5	10.2	675	21	W71195	Human Heregulin HR	930	5	10.2	686	21	G32087	Arabidopsis thalia
858	5	10.2	675	21	W71196	Human Heregulin HR	931	5	10.2	689	19	W98483	H. pylori GHP0 992
859	5	10.2	675	21	W71197	Human Heregulin HR	932	5	10.2	690	21	G30548	Arabidopsis thalia
860	5	10.2	675	21	W71198	Human Heregulin HR	933	5	10.2	692	21	G30390	Arabidopsis thalia
861	5	10.2	675	21	W71199	Human Heregulin HR	934	5	10.2	693	21	G32091	Arabidopsis thalia
862	5	10.2	675	21	W71200	Human Heregulin HR	935	5	10.2	699	21	G16607	Arabidopsis thalia
863	5	10.2	675	21	W71201	Human Heregulin HR	936	5	10.2	699	21	G49525	Arabidopsis thalia
864	5	10.2	675	21	W71202	Human Heregulin HR	937	5	10.2	702	14	R40810	ADA3. Synthetic.
865	5	10.2	675	21	W71203	Human Heregulin HR	938	5	10.2	704	12	R14204	Cyclodextrin gluca
866	5	10.2	677	19	W55984	Swinepox virus str	939	5	10.2	704	12	R15313	Cyclodextrin gluca
867	5	10.2	679	17	W17650	CGTase variant 87-	940	5	10.2	704	12	R15314	Cyclodextrin gluca
868	5	10.2	679	17	W17652	CGTase variant 87-	941	5	10.2	704	12	R11217	Cyclodextrin gluca
869	5	10.2	681	17	W17607	Thermoanaerobacter	942	5	10.2	704	14	R41248	B.ohbensis mutant
870	5	10.2	681	17	W17615	Thermoanaerobacter	943	5	10.2	704	14	R41249	B.ohbensis Alai88
871	5	10.2	682	17	W17638	CGTase variant 87-	944	5	10.2	704	14	R41250	B.ohbensis Ser188
872	5	10.2	682	17	W17639	CGTase variant F19	945	5	10.2	704	14	R41251	B.ohbensis Trp188
873	5	10.2	682	17	W17649	CGTase variant 87-	946	5	10.2	722	20	W86308	Kidney injury asso
874	5	10.2	682	17	W17606	Thermoanaerobacter	947	5	10.2	722	21	G51802	Arabidopsis thalia
875	5	10.2	682	17	W17608	Thermoanaerobacter	948	5	10.2	725	21	G38851	Arabidopsis thalia
876	5	10.2	682	17	W17609	CGTase variant F19	949	5	10.2	728	21	G49524	Arabidopsis thalia
877	5	10.2	682	17	W17611	CGTase variant 87-	950	5	10.2	729	21	G16606	Arabidopsis thalia
878	5	10.2	682	17	W17612	CGTase variant 87-	951	5	10.2	730	21	G32090	Arabidopsis thalia
879	5	10.2	682	17	W17637	Thermoanaerobacter	952	5	10.2	734	21	G38557	Arabidopsis thalia
880	5	10.2	682	21	G25645	Arabidopsis thalia	953	5	10.2	740	20	Y25005	Meion MEETRI prote
881	5	10.2	682	21	G51608	Arabidopsis thalia	954	5	10.2	741	21	G38556	Arabidopsis thalia
882	5	10.2	683	17	W06772	Wild type cyclomal	955	5	10.2	746	20	Y28882	Human Ext-1 protei
883	5	10.2	683	17	W17640	Thermoanaerobacter	956	5	10.2	763	20	Y04741	PDZ domain-contain
884	5	10.2	683	17	W17641	Thermoanaerobacter	957	5	10.2	767	19	Y11030	H. pylori ORF Olcp
885	5	10.2	683	17	W17642	Thermoanaerobacter	958	5	10.2	767	20	Y17184	H. pylori outer me
886	5	10.2	683	17	W17643	Thermoanaerobacter	959	5	10.2	768	19	W44817	Human gamma-heregu
887	5	10.2	683	17	W17644	Thermoanaerobacter	960	5	10.2	768	20	Y06639	Gamma-heregulin.



CC		also be used to identify compounds able to inhibit binding of RSV to host					
CC		cells and for characterisation of cell receptors for Pneumoviruses. When					
CC		the fragments are used in combination with existing vaccines, they may					
XX		allow a reduction in dose, and thus side effects, of the vaccine.					
XX	SQ	Sequence		49 AA;			
		Query Match	100.0%;	Score 49;	DB 19; Length 49;		
		Best Local Similarity	100.0%;	Pred. No. 1.4e-43;			
		Matches 49;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY		1 KORONKPPSKNNDFHEVFNFVPCISCSNPTCWAICKRIPNKYPGKK 49 					
Dd		1 kqrqnpkspndfhfevfncfscnptcwaickripnkypgkk 49 					
	RESULT	4					
W39250	ID	W39250 standard; peptide; 49 AA.					
XX	AC	W39250;					
XX	DT	27-AUG-1998 (first entry)					
XX	XX	Human RSV G protein fragment (aa. 149-157) derivative #7.					
DE	XX						
KW	XX	G protein; treatment; prevention; diagnosis; infection; immunity; antibody; Pneumovirus; identification; vaccine; cell receptor.					
KX	OS	Human respiratory syncytial virus.					
XX	Key	Location/Qualifiers					
FH	Modified-site	1 /note= "N-terminal bb group"					
FT	Disulfide-bond	25..38					
FT	Disulfide-bond	28..34					
FT	Modified-site	49 /note= "C-terminal amide"					
FT							
PN	WO9746581-A1.						
XX	XX	11-DEC-1997.					
PD	XX	04-JUN-1997; 97WO-AU000351.					
PF	XX	05-JUN-1996; 96AU-0000265.					
PR	XX	(BIOM-) BIOMOLECULAR RES INST LTD.					
XX	PA	Gorman JJ;					
XX	PI	WPI; 1998-042117/04.					
XX	DR						
XX	PT	Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection					
PS	Example	4; Fig 12; 75pp; English.					
XX	CC	W39244-W39252 are derivatives of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to identify compounds able to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.					
XX	SQ	Sequence		49 AA;			

Query Match 100.0%; Score 49; DB 19; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.4e-43;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNNDFEFVPCISNNPTCWAICKRIPNKKPGKK 49  
|||||  
DB 1 kqrqkpskpndthfevfnvpcisnptcwaickripnkkpgkk 49

RESULT 5  
W39251  
ID W39251 standard; peptide; 49 AA.  
XX  
AC W39251;  
XX  
DT 27-AUG-1998 (first entry)  
XX  
DE Human RSV G protein fragment (aa. 149-157) derivative #8.  
XX  
KW G protein; treatment; prevention; diagnosis; infection; immunity;  
KW antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX  
OS Human respiratory syncytial virus.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal biot group"  
FT Disulfide-bond 25..38  
FT Disulfide-bond 28..34  
FT Modified-site 49  
FT /note= "C-terminal amide"  
XX  
XX WO9746581-A1.  
XX  
XX 11-DEC-1997.  
XX  
XX 04-JUN-1997; 97WO-AU00351.  
XX  
XX 05-JUN-1996; 96AU-0000265.  
XX  
XX (BIOM-) BIOMOLECULAR RES INST LTD.  
XX  
XX Goldman JJ;  
XX  
XX WPI; 1998-042117/04.  
XX  
XX Peptide(s) derived from specific region of respiratory syncytial  
XX virus G protein - used to treat, prevent, diagnose and immunise  
XX against Pneumovirus infection  
XX  
XX Example 4; Fig 12; 75pp; English.  
XX  
XX W39244-W39252 are derivatives of the human respiratory syncytial virus  
XX (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
XX can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
XX infection and to immunise against such infections. Antibodies raised  
XX from these fragments may also be used diagnostically. The fragments may  
XX also be used to identify compounds able to inhibit binding of RSV to host  
XX cells and for characterisation of cell receptors for Pneumoviruses. When  
XX the fragments are used in combination with existing vaccines, they may  
XX allow a reduction in dose, and thus side effects, of the vaccine.  
XX  
XX Sequence 49 AA;

Query Match 100.0%; Score 49; DB 19; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.4e-43;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNNDFEFVPCISNNPTCWAICKRIPNKKPGKK 49  
|||||  
DB 1 kqrqkpskpndthfevfnvpcisnptcwaickripnkkpgkk 49

RESULT 6  
P70845  
ID P70845 standard; protein; 298 AA.  
XX  
AC P70845;  
XX  
DT 05-APR-1991 (first entry)  
XX  
DE Sequence of human respiratory syncytial virus (HRSV) A2 strain  
DE G protein.  
XX  
KW Vaccine.  
XX  
OS Human respiratory syncytial virus (HRSV).  
XX  
PN W08704185-A  
PD 16-JUL-1987.  
XX  
PF 23-DEC-1986; 86WO-US02756.  
XX  
PR 14-JAN-1986; 86US-0818740.  
XX  
PA (UXNC-) UNIV OF N CAROLINA.  
PA (WERTZ) WERTZ G W.  
XX (WERTZ) WERTZ G W.  
XX WPI; 1987-206300/29.  
DR N-PSDB; N70784.  
XX  
XX Vaccines for human respiratory virus - comprising proteins or  
XX fragment encoded by a DNA sequence coding for human respiratory  
XX syncytial virus proteins.  
XX  
XX Disclosure; Chart 13; 57pp; English.  
XX  
XX A novel plasmid which comprises a DNA sequence encoding this  
XX protein, and the protein itself, are claimed, for use as HRSV  
XX vaccines. The vaccine can be administered to pregnant women or to  
XX women of child bearing age to stimulate maternal antibodies.  
XX Infants can also be vaccinated at 2-3 months of age.  
XX  
XX Sequence 298 AA.

Query Match 100.0%; Score 49; DB 8; Length 298;  
Best Local Similarity 100.0%; Pred. No. 5.7e-43;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNNDFEFVPCISNNPTCWAICKRIPNKKPGKK 49  
|||||  
DB 149 kqrqkpskpndthfevfnvpcisnptcwaickripnkkpgkk 197

RESULT 7  
R25302  
ID R25302 standard; Protein; 298 AA.  
XX  
AC R25302;  
XX  
DT 03-MAR-1993 (first entry)  
XX  
DE HSRV glycoprotein G (gpc).  
XX  
KW Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K;  
KW major capsid protein; N.  
XX  
OS Human respiratory syncytial virus strain A2.  
XX  
PN U55149650-A  
XX  
XX 22-SEP-1992.

XX 14-JAN-1986; 86US-0818740.  
XX  
XX 14-JAN-1986; 86US-0818740.  
PR 13-JUL-1988; 88US-0218737.  
XX  
XX (UYN-) UNIV NORTH CAROLINA.  
XX  
XX Collins PL, Wertz GW;  
PI  
XX WPI: 1992-340247/41.  
DR N-PSDB; Q29623.  
XX  
XX Vaccines for human respiratory virus - include structural genes  
PT coding for native structural viral proteins and immunogenic  
PT fragments  
XX  
XX Disclosure; Page 18; 21pp; English.  
XX  
XX The sequences of mRNA encoding HRSV structural proteins are given in  
CC Q29622-26. The proteins are F, G, 22K, 9.5K and major capsid  
CC protein N. The sequences and encoded proteins are useful for  
CC preparing vaccines against HRSV. The vaccines can be used to confer  
CC immunity against respiratory tract infections on human subjects.  
XX  
XX Sequence 298 AA;  
SQ

Query Match 100.0%; Score 49; DB 13; Length 298;  
Best Local Similarity 100.0%; Pred. No. 5.7e-43;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDHFHVFVPCISCSNNPTCWAICKRIPNKKPGKK 49  
|||||  
Db 149 kqrqkppskpndhfefvfnfpcisnntcwaickripnkkpgkk 197

RESULT 8  
W47605  
ID W47605 standard; Protein; 298 AA.  
XX  
XX W47605;  
XX  
XX 11-JUN-1998 (first entry)  
XX  
XX HRSV glycoprotein G.  
XX  
XX HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine.  
XX  
XX Human respiratory syncytial virus.  
XX  
XX US5716823-A.  
PN  
XX  
XX 10-FEB-1998.  
PD  
XX  
XX 12-MAY-1997; 97US-0854783.  
PF  
XX  
XX 13-JUL-1988; 86US-0218737.  
XX  
XX 14-JAN-1986; 86US-0818740.  
PR 23-DEC-1986; 86WO-US02756.  
PR 11-JUN-1992; 92US-0897171.  
PR 12-MAY-1997; 97US-0854783.  
XX  
XX (PHAA ) PHARMACIA & UPJOHN CO.  
PA  
XX Collins PL, Wertz GW;  
PI  
XX WPI: 1998-144802/13.  
DR N-PSDB; V18736.  
XX  
XX Production of human respiratory syncytial virus glyco-protein F or G  
PT - by culturing eukaryotic host cells transfected with corresponding  
PT DNA.

XX Example 1; Columns 27-38; 17pp; English.  
XX  
XX The present sequence was used in the development of a novel method  
CC for the production of human respiratory syncytial virus (HRSV)  
CC glycoprotein F (gpF) or glycoprotein G (gpG). The method comprises  
CC culturing eukaryotic host cells transfected with an isolated DNA  
CC sequence encoding HRSV gpF or gpG. The gp can be used to prepare  
XX vaccines against HRSV.  
XX  
XX Sequence 298 AA;  
SQ

Query Match 100.0%; Score 49; DB 19; Length 298;  
Best Local Similarity 100.0%; Pred. No. 5.7e-43;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDHFHVFVPCISCSNNPTCWAICKRIPNKKPGKK 49  
|||||  
Db 149 kqrqkppskpndhfefvfnfpcisnntcwaickripnkkpgkk 197

RESULT 9  
P90441  
ID P90441 standard; Protein; 681 AA.  
XX  
XX P90441;  
XX  
XX 01-NOV-1989 (first entry)  
XX  
XX Chimeric human respiratory syncytial virus glycoproteins F and G.  
XX  
XX Chimeric polypeptide; human respiratory syncytial virus;  
KW protein F; protein G; vaccine.  
XX  
XX Human respiratory syncytial virus.  
XX  
XX WO8905823-A.  
PN  
XX  
XX 29-JUN-1989.  
PD  
XX  
XX 31-OCT-1988; 88WO-US03784.  
PF  
XX  
XX 23-DEC-1987; 87US-0137387.  
PR  
XX  
XX (UPJO ) UPJOHN CO.  
PA  
XX  
XX Nathen M;  
PI  
XX  
XX WPI: 1989-206593/28.  
DR  
XX  
XX Chimeric human respiratory syncytial virus polypeptides(s)  
PT - contg. immunogenic fragments from HRSV glycoproteins  
PT F and G, for vaccine prodn.  
PT  
XX  
XX Claim 3; page 47-48; 50pp; English.  
PS  
XX  
XX Chimeric polypeptide contg. a signal sequence and one or more  
CC immunogenic fragments from both human respiratory syncytial virus  
CC glycoproteins F and G. Can be used in vaccines. Hosts are, eg  
CC E. coli, Chinese hamster ovary cells, murine C127 cells and  
CC S. frugiperda.  
XX  
XX Sequence 681 AA;  
SQ

Query Match 100.0%; Score 49; DB 10; Length 681;  
Best Local Similarity 100.0%; Pred. No. 1.1e-42;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDHFHVFVPCISCSNNPTCWAICKRIPNKKPGKK 49  
|||||  
Db 543 kqrqkppskpndhfefvfnfpcisnntcwaickripnkkpgkk 591

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RESULT 10
W39219 ID W39219 standard; peptide; 49 AA.
XX AC W39219;
XX AC
DT 27-AUG-1998 (first entry)
XX DE Human RSV A subtype G protein fragment (aa. 149-157) strain A642.
XX KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX OS Human respiratory syncytial virus.
XX FH Key Location/Qualifiers
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX PN WO9746581-A1.
XX PD 11-DEC-1997.
XX PF 04-JUN-1997; 97WO-AU00351.
XX PR 05-JUN-1996; 96AU-0000265.
XX PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX PI Gorman JJ;
XX DR WPI; 1998-042117/04.
XX PT Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX PS Claim 5; Fig 2; 75pp; English.
XX SQ Sequence 49 AA;
CC W39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to host
CC cells and for characterisation of cell receptors for Pneumoviruses. When
CC the fragments are used in combination with existing vaccines, they may
CC allow a reduction in dose, and thus side effects, of the vaccine.
XX SQ Sequence 49 AA;

Query Match 98.0%; Score 48; DB 19; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNNDFFHFVFNPCISCSNNPTCWAICKRIPNKKPGK 48
Db 1 kqrqkppskpndffhfvfnpciscsnnptcwaickripnkkpgk 48

RESULT 12
W39220 ID W39220 standard; peptide; 49 AA.
XX AC W39220;
XX AC
DT 27-AUG-1998 (first entry)
XX DE Human RSV A subtype G protein fragment (aa. 149-157) strain A6614.
XX KW G protein; treatment; prevention; diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX OS Human respiratory syncytial virus.
XX FH Key Location/Qualifiers
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
XX PN WO9746581-A1.
XX PD 11-DEC-1997.

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XX PF 04-JUN-1997; 97WO-AU00351.
XX PR 05-JUN-1996; 96AU-0000265.
XX PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX PI Gorman JJ;
XX DR WPI; 1998-042117/04.
XX PT Peptide(s) derived from specific region of respiratory syncytial
XX PT virus G protein - used to treat, prevent, diagnose and immunise
XX PT against Pneumovirus infection
XX PS Claim 5; Fig 2; 75pp; English.
XX CC W39217-W39234 are fragments of the human respiratory syncytial virus
XX CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
XX CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
XX CC infection and to immunise against such infections. Antibodies raised
XX CC from these fragments may also be used diagnostically. The fragments may
XX CC also be used to identify compounds able to inhibit binding of RSV to host
XX CC cells and for characterisation of cell receptors for Pneumoviruses. When
XX CC the fragments are used in combination with existing vaccines, they may
XX CC allow a reduction in dose, and thus side effects, of the vaccine.
XX SQ Sequence 49 AA;
Query Match 93.9%; Score 46; DB 19; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 QNKPKPNNDHFHFVPCISCSNNPTCWAICKRIPNKKPGKK 49
DB 4 qnkpskpndhfefvpcisnnpctwaickripnkkpgkk 49
RESULT 13
W39245
ID W39245 standard; peptide; 42 AA.
AC W39245;
XX 27-AUG-1998 (first entry)
XX DE Human RSV G protein fragment (aa. 149-157) derivative #2.
XX KW G protein; treatment; prevention; diagnosis; infection; immunity;
XX KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX OS Human respiratory syncytial virus.
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetylated"
FT Disulfide-bond 25..38
FT Disulfide-bond 28..34
FT Modified-site 42
FT FT /note= "C-terminal amide"
XX
XX WO9746581-A1.
XX PN
XX PD 11-DEC-1997.
XX PF 04-JUN-1997; 97WO-AU00351.
XX PR 05-JUN-1996; 96AU-0000265.
XX PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
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PI Gorman JJ;
XX DR WPI; 1998-042117/04.
XX PT Peptide(s) derived from specific region of respiratory syncytial
XX PT virus G protein - used to treat, prevent, diagnose and immunise
XX PT against Pneumovirus infection
XX PS Example 4; Fig 12; 75pp; English.
XX CC W39244-W39252 are derivatives of the human respiratory syncytial virus
XX CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
XX CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
XX CC infection and to immunise against such infections. Antibodies raised
XX CC from these fragments may also be used diagnostically. The fragments may
XX CC also be used to identify compounds able to inhibit binding of RSV to host
XX CC cells and for characterisation of cell receptors for Pneumoviruses. When
XX CC the fragments are used in combination with existing vaccines, they may
XX CC allow a reduction in dose, and thus side effects, of the vaccine.
XX SQ Sequence 42 AA;
Query Match 85.7%; Score 42; DB 19; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e-36;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KORQNKPPKPNNDHFHFVPCISCSNNPTCWAICKRIP 42
DB 1 kqrqnkpskpndhfefvpcisnnpctwaickrip 42
RESULT 14
W97304
ID W97304 standard; Peptide; 43 AA.
XX AC W97304;
XX DT 26-MAY-1999 (first entry)
XX DE Peptide which induces the antibodies of the invention.
XX KW Antibody; epitope; protein G; respiratory syncytial virus; RSV;
XX KW RSV-related disease.
XX OS Synthetic.
XX PN WO9903987-A2.
XX PD 28-JAN-1999.
XX PF 17-JUL-1998; 98WO-FR01570.
XX PR 17-JUL-1997; 97FR-0009079.
XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.
XX PI Beck A, Goestch L, Nguyen TN, Power U;
XX DR WPI; 1999-132232/11.
XX DR N-PSDB; X15813.
XX PT New antibodies directed against epitopes in protein G of respiratory
XX PT syncytial virus - used for treatment, prevention and diagnosis of
XX PT RSV infections
XX PS Claim 3; Page 51; 54pp; French.
XX CC The present sequence represents a peptide which induces the antibodies
XX CC of the invention. The specification describes mono- or poly-clonal
XX CC antibodies that are directed against an epitope that corresponds to
XX CC amino acids 150-159, 176-189, 194-207 or 153-176 of protein G of
XX CC respiratory syncytial virus (RSV), subgroups A or B. The antibodies
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CC are used for treating, preventing (passive or active immunisation)  
CC and diagnosing RSV-related diseases, including differentiating between  
CC infection by subgroups A or B.  
XX  
SQ Sequence 43 AA;

Query Match 81.6%; Score 40; DB 20; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2.3e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 KPNNDFHEVFVPCSCSNPTCWAICKRIPNKKPGKK 49  
Db 1 kpndfhfevfvpvpcscsnptcwaickripnkkpgkk 40

RESULT 15

W39218  
ID W39218 standard; peptide; 49 AA.  
XX  
AC W39218;  
XX  
DT 27-AUG-1998 (first entry)  
XX  
DE Human RSV A subtype G protein fragment (aa 149-157) strain long A.  
XX  
KW G protein; treatment; prevention; diagnosis; infection; immunity;  
XX antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX  
OS Human respiratory syncytial virus.

FH Key Location/Qualifiers  
FT Disulfide-bond 25..38  
ET Disulfide-bond 28..34  
XX  
FN WO9746581-A1.

XX  
XX 11-DEC-1997.  
XX  
XX 04-JUN-1997; 97WO-AU00351.  
XX  
XX 05-JUN-1996; 96AU-0000265.  
XX  
XX (BIOM-) BIOMOLECULAR RES INST LTD.  
XX  
XX Gorman JJ;  
XX  
XX WPI; 1998-042117/04.

PT Peptide(s) derived from specific region of respiratory syncytial  
PT virus G protein - used to treat, prevent, diagnose and immunise  
PT against Pneumovirus infection  
XX

PS Claim 5; Fig 2; 75pp; English.

XX  
XX  
CC W39217-W39234 are fragments of the human respiratory syncytial virus  
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to host  
CC cells and for characterisation of cell receptors for Pneumoviruses. When  
CC the fragments are used in combination with existing vaccines, they may  
CC allow a reduction in dose, and thus side effects, of the vaccine.

XX Sequence 49 AA;

Query Match 81.6%; Score 40; DB 19; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.6e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 KPNNDFHEVFVPCSCSNPTCWAICKRIPNKKPGKK 49

Db 10 kpndfhfevfvpvpcscsnptcwaickripnkkpgkk 49

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Job time: 93 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:16:32 ; Search time 11.77 Seconds  
(without alignments)  
79.977 Million cell updates/sec

Title: US-09-202-035-1  
Perfect score: 49  
Sequence: 1 KORQKPPSKPNNDHFHFEV.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 185757 seqs, 19210857 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	40	81.6	298	2	US-08-467-963C-8
3	40	81.6	298	2	US-08-838-189D-8
4	40	81.6	298	3	US-08-852-344D-8
5	40	81.6	298	3	US-08-344-639E-8
6	40	81.6	298	4	US-08-467-969A-8
7	40	81.6	298	4	US-08-467-961A-8
8	36	73.5	37	3	US-08-793-792-12
9	32	65.3	32	3	US-08-793-792-8
10	28	57.1	28	3	US-08-793-792-4
11	16	32.7	16	3	US-08-793-792-13
12	13	26.5	28	3	US-08-793-792-3
13	13	26.5	32	3	US-08-793-792-7
14	13	26.5	37	3	US-08-793-792-11
15	12	24.5	30	4	US-08-836-504A-5
16	12	24.5	30	4	US-08-836-504A-6
17	6	12.2	28	2	US-08-451-371-1
18	6	12.2	28	2	US-08-451-371-2
19	6	12.2	28	2	US-08-451-371-3
20	6	12.2	28	2	US-08-451-371-4
21	6	12.2	28	2	US-08-451-371-5
22	5	10.2	9	2	US-08-586-764-2
23	5	10.2	9	6	5368712-5
24	5	10.2	11	4	US-09-224-785-31
25	5	10.2	14	4	US-08-721-979A-9
26	5	10.2	14	4	US-08-721-979A-11
27	5	10.2	14	4	US-08-836-501-9

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Sequence 20, Appl	US-08-836-501-20	17	4
Sequence 3, Appl	US-07-855-412B-3	18	1
Sequence 3, Appl	US-08-308-887A-3	18	2
Sequence 3, Appl	US-08-881-094-3	18	3
Sequence 10, Appl	US-08-597-495B-10	21	1
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Sequence 4, Appl	US-09-282-351A-4	22	4
Sequence 19, Appl	US-09-282-351A-19	22	4
Sequence 20, Appl	US-09-282-351A-20	22	4
Sequence 44, Appl	US-09-282-351A-44	22	4
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Sequence 46, Appl	US-09-282-351A-46	22	4
Sequence 47, Appl	US-09-282-351A-47	22	4
Sequence 48, Appl	US-09-282-351A-48	22	4
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Sequence 11, Appl	US-08-290-919-11	106	1
Sequence 5, Appl	US-09-083-351-5	106	3
Sequence 6, Appl	US-09-083-351-6	106	3
Sequence 5, Appl	US-09-083-352-5	106	4
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Sequence 20, Appl	US-09-088-697A-20	117	4
Sequence 7, Appl	US-08-489-666C-7	121	2
Sequence 7, Appl	US-08-911-092-7	121	2
Sequence 7, Appl	US-08-485-001B-7	121	2
Sequence 7, Appl	US-08-454-121A-7	121	3
Sequence 7, Appl	US-08-482-161B-7	121	4
Sequence 36, Appl	US-08-188-091A-36	122	1
Sequence 10, Appl	US-09-008-697A-10	125	4
Sequence 98, Appl	US-08-836-561-98	127	3
Sequence 103, Appl	US-08-836-561-103	127	3
Sequence 35, Appl	US-08-168-091A-35	139	1
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Sequence 18, Appl	US-08-096-277-18	161	1
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Sequence 33, Appl	US-08-168-091A-33	165	1
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Sequence 6, Appl	US-07-929-198-4	226	1
Sequence 6, Appl	US-07-929-198-6	226	1
Sequence 15, Appl	US-08-557-146-15	226	2
Sequence 15, Appl	US-09-154-344-15	226	2
Sequence 26, Appl	PCT-US94-01149-26	226	5
Sequence 30, Appl	US-07-847-743B-30	241	1
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Sequence 30, Appl	US-08-456-241-30	241	1
Sequence 9, Appl	PCT-US92-04295A-30	241	5
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Sequence 21, Appl	US-08-729-416C-21	260	3
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Sequence 4, Appl	US-08-808-148-4	281	3

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106	5	10.2	311	4	US-09-008-697A-22	Sequence 22, Appli	179	5	10.2	601	4	US-08-470-335-233	Sequence 233, App
107	5	10.2	319	1	US-08-597-495B-22	Sequence 22, Appli	180	5	10.2	603	2	US-08-687-865A-2	Sequence 2, Appli
108	5	10.2	319	4	US-09-008-697A-6	Sequence 6, Appli	181	5	10.2	604	4	US-08-470-335-227	Sequence 227, App
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116	5	10.2	359	4	US-09-008-697A-14	Sequence 14, Appli	189	5	10.2	620	2	US-08-852-153-2	Sequence 2, Appli
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125	5	10.2	420	1	US-08-456-201-29	Sequence 29, Appli	198	5	10.2	637	5	PCT-US92-04295A-28	Sequence 28, Appli
126	5	10.2	420	1	US-08-456-241-29	Sequence 29, Appli	199	5	10.2	638	4	US-08-470-335-240	Sequence 240, App
127	5	10.2	420	5	PCT-US92-04295A-29	Sequence 29, Appli	200	5	10.2	644	4	US-08-470-335-250	Sequence 250, App
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129	5	10.2	422	1	US-08-469-569-170	Sequence 170, App	202	5	10.2	645	1	US-08-456-201-27	Sequence 27, Appli
130	5	10.2	422	1	US-08-428-948-3	Sequence 3, Appli	203	5	10.2	645	1	US-08-428-926-4	Sequence 4, Appli
131	5	10.2	422	1	US-08-249-322A-170	Sequence 170, App	204	5	10.2	645	1	US-08-428-927-4	Sequence 4, Appli
132	5	10.2	422	1	US-08-428-927-3	Sequence 3, Appli	205	5	10.2	645	1	US-08-438-298-4	Sequence 4, Appli
133	5	10.2	422	1	US-08-428-298-3	Sequence 3, Appli	206	5	10.2	645	1	US-08-339-517-4	Sequence 4, Appli
134	5	10.2	422	1	US-08-339-517-3	Sequence 3, Appli	207	5	10.2	645	2	US-08-456-241-27	Sequence 27, Appli
135	5	10.2	422	1	US-08-469-526A-170	Sequence 170, App	208	5	10.2	645	3	US-08-753-007A-10	Sequence 10, Appli
136	5	10.2	422	2	US-08-734-591A-170	Sequence 170, App	209	5	10.2	645	4	US-09-398-496-10	Sequence 10, Appli
137	5	10.2	422	2	US-08-469-660-170	Sequence 170, App	210	5	10.2	645	4	US-09-020-880-93	Sequence 93, Appli
138	5	10.2	422	3	US-08-753-007A-9	Sequence 9, Appli	211	5	10.2	645	5	PCT-US92-04295A-27	Sequence 27, Appli
139	5	10.2	422	3	US-08-341-018-72	Sequence 72, Appli	212	5	10.2	647	4	US-08-470-335-243	Sequence 243, App
140	5	10.2	422	4	US-09-398-496-9	Sequence 9, Appli	213	5	10.2	664	2	US-08-852-153-8	Sequence 8, Appli
141	5	10.2	422	4	US-08-470-335-170	Sequence 170, App	214	5	10.2	669	1	US-07-847-743B-8	Sequence 8, Appli
142	5	10.2	422	4	US-08-735-021-170	Sequence 170, App	215	5	10.2	669	1	US-07-847-743B-13	Sequence 13, Appli
143	5	10.2	422	4	US-08-734-664A-170	Sequence 170, App	216	5	10.2	669	1	US-08-456-201-8	Sequence 8, Appli
144	5	10.2	422	5	PCT-US94-05083C-166	Sequence 166, App	217	5	10.2	669	1	US-08-456-201-13	Sequence 13, Appli
145	5	10.2	422	5	PCT-US94-05083C-185	Sequence 185, App	218	5	10.2	669	2	US-08-330-161-11	Sequence 11, Appli
146	5	10.2	422	5	PCT-US95-06846A-170	Sequence 170, App	219	5	10.2	669	2	US-08-456-241-8	Sequence 8, Appli
147	5	10.2	425	4	US-08-470-335-226	Sequence 226, App	220	5	10.2	669	2	US-08-456-241-13	Sequence 13, Appli
148	5	10.2	451	1	US-08-417-330A-12	Sequence 12, Appli	221	5	10.2	669	2	US-08-440-401-11	Sequence 11, Appli
149	5	10.2	456	2	US-09-018-628-16	Sequence 16, Appli	222	5	10.2	669	2	US-08-419-878B-11	Sequence 11, Appli
150	5	10.2	456	2	US-08-910-731-4	Sequence 4, Appli	223	5	10.2	669	5	PCT-US92-04295A-8	Sequence 8, Appli
151	5	10.2	456	2	US-08-795-395-4	Sequence 4, Appli	224	5	10.2	669	5	PCT-US92-04295A-13	Sequence 13, Appli
152	5	10.2	456	3	US-09-273-378-16	Sequence 16, Appli	225	5	10.2	675	3	US-08-947-965-76	Sequence 76, Appli
153	5	10.2	456	3	US-08-470-335-246	Sequence 246, App	226	5	10.2	677	3	US-08-480-640A-115	Sequence 115, App
154	5	10.2	459	4	US-08-470-335-239	Sequence 239, App	227	5	10.2	677	3	US-08-480-640A-193	Sequence 193, App
155	5	10.2	474	2	US-08-185-828A-12	Sequence 12, Appli	228	5	10.2	677	4	US-08-295-802-115	Sequence 115, App
156	5	10.2	474	2	US-08-185-828A-18	Sequence 18, Appli	229	5	10.2	683	3	US-08-947-965-2	Sequence 2, Appli
157	5	10.2	474	3	US-08-185-828A-24	Sequence 24, Appli	230	5	10.2	685	3	US-08-947-965-74	Sequence 74, Appli
158	5	10.2	474	3	US-08-729-416C-1	Sequence 1, Appli	231	5	10.2	732	1	US-07-847-743B-9	Sequence 9, Appli
159	5	10.2	474	3	US-08-729-416C-11	Sequence 11, Appli	232	5	10.2	732	1	US-08-456-201-9	Sequence 9, Appli
160	5	10.2	474	3	US-08-807-342B-2	Sequence 2, Appli	233	5	10.2	732	2	US-08-456-241-9	Sequence 9, Appli
161	5	10.2	481	4	US-08-943-714-10	Sequence 10, Appli	234	5	10.2	732	5	PCT-US92-04295A-9	Sequence 9, Appli
162	5	10.2	491	1	US-08-360-673-4	Sequence 4, Appli	235	5	10.2	768	3	US-08-891-845-2	Sequence 2, Appli
163	5	10.2	498	5	PCT-US94-01101-2	Sequence 2, Appli	236	5	10.2	777	1	US-08-526-964-3	Sequence 3, Appli
164	5	10.2	500	3	US-09-018-628-18	Sequence 18, Appli	237	5	10.2	777	2	US-08-946-617-3	Sequence 3, Appli
165	5	10.2	500	3	US-09-273-378-18	Sequence 18, Appli	238	5	10.2	777	3	US-09-031-897-3	Sequence 3, Appli
166	5	10.2	501	2	US-08-969-630-4	Sequence 4, Appli	239	5	10.2	793	3	US-08-374-077C-4	Sequence 4, Appli
167	5	10.2	501	3	US-08-891-845-10	Sequence 10, Appli	240	5	10.2	793	4	US-08-895-590-4	Sequence 4, Appli
168	5	10.2	502	2	US-08-969-630-2	Sequence 2, Appli	241	5	10.2	798	2	US-07-728-215-30	Sequence 30, Appli
169	5	10.2	529	2	US-08-933-227-4	Sequence 4, Appli	242	5	10.2	818	4	US-08-470-335-234	Sequence 234, App
170	5	10.2	553	3	US-09-083-351-2	Sequence 2, Appli	243	5	10.2	821	4	US-08-470-335-228	Sequence 228, App
171	5	10.2	553	4	US-09-083-352-2	Sequence 2, Appli	244	5	10.2	827	4	US-08-470-335-237	Sequence 237, App
172	5	10.2	577	2	US-08-852-153-4	Sequence 4, Appli	245	5	10.2	830	4	US-08-470-335-231	Sequence 231, App
173	5	10.2	586	6	5256558-2	Patent No. 5256558	246	5	10.2	852	4	US-08-470-335-248	Sequence 248, App

247	5	10.2	855	4	US-08-470-335-241	Sequence 241, App	320	4	8.2	15	2	US-08-436-717-121	Sequence 121, App
248	5	10.2	861	4	US-08-470-335-251	Sequence 251, App	321	4	8.2	15	2	US-08-436-717-140	Sequence 140, App
249	5	10.2	864	4	US-08-470-335-244	Sequence 244, App	322	4	8.2	15	2	US-08-582-298-13	Sequence 13, Appl
250	5	10.2	865	4	US-08-470-335-235	Sequence 235, App	323	4	8.2	15	2	US-08-248-839C-152	Sequence 152, App
251	5	10.2	868	4	US-08-470-335-229	Sequence 229, App	324	4	8.2	15	2	US-08-553-501A-66	Sequence 66, Appl
252	5	10.2	874	4	US-08-470-335-238	Sequence 238, App	325	4	8.2	15	2	US-08-553-501A-70	Sequence 70, Appl
253	5	10.2	877	4	US-08-470-335-232	Sequence 232, App	326	4	8.2	15	2	US-08-687-956A-5	Sequence 5, Appl
254	5	10.2	899	4	US-08-470-335-249	Sequence 249, App	327	4	8.2	15	2	US-08-318-157B-27	Sequence 27, Appl
255	5	10.2	905	4	US-08-470-335-242	Sequence 242, App	328	4	8.2	15	2	US-09-086-201-20	Sequence 20, Appl
256	5	10.2	902	4	US-08-074-658-70	Sequence 70, Appl	329	4	8.2	15	2	US-08-765-783A-88	Sequence 88, Appl
257	5	10.2	908	4	US-08-470-335-252	Sequence 252, App	330	4	8.2	15	2	US-08-470-139-11	Sequence 11, Appl
258	5	10.2	911	4	US-08-470-335-245	Sequence 245, App	331	4	8.2	15	2	US-08-470-139-12	Sequence 12, Appl
259	5	10.2	1027	4	US-08-446-137B-2	Sequence 2, Appl	332	4	8.2	15	4	US-08-649-100-28	Sequence 28, Appl
260	5	10.2	1144	2	US-08-147-812-5	Sequence 12, Appl	333	4	8.2	15	4	US-09-205-231-66	Sequence 66, Appl
261	5	10.2	1144	2	US-08-319-866-12	Sequence 12, Appl	334	4	8.2	15	4	US-09-205-231-70	Sequence 70, Appl
262	5	10.2	1144	4	US-09-123-708-2	Sequence 2, Appl	335	4	8.2	15	4	US-08-569-147-38	Sequence 38, Appl
263	5	10.2	1144	4	US-09-123-624-2	Sequence 2, Appl	336	4	8.2	15	4	US-08-875-309-15	Sequence 15, Appl
264	5	10.2	1253	1	US-07-920-281C-3	Sequence 3, Appl	337	4	8.2	15	5	PCT-US95-11405-7	Sequence 7, Appl
265	5	10.2	1253	4	US-08-466-277-3	Sequence 3, Appl	338	4	8.2	15	5	PCT-US95-11405-13	Sequence 13, Appl
266	5	10.2	1264	1	US-07-789-915A-6	Sequence 6, Appl	339	4	8.2	16	1	US-07-609-716-6	Sequence 6, Appl
267	5	10.2	1264	1	US-08-005-002C-6	Sequence 6, Appl	340	4	8.2	16	1	US-07-794-288D-40	Sequence 40, Appl
268	5	10.2	1264	1	US-08-487-203A-6	Sequence 6, Appl	341	4	8.2	16	1	US-07-942-245-71	Sequence 71, Appl
269	5	10.2	1732	2	US-08-477-451-14	Sequence 14, Appl	342	4	8.2	16	1	US-07-942-245-72	Sequence 72, Appl
270	5	10.2	1781	2	US-08-477-451-11	Sequence 11, Appl	343	4	8.2	16	1	US-07-942-245-73	Sequence 73, Appl
271	5	10.2	1872	6	5386025-6	Patent No. 5386025	344	4	8.2	16	1	US-07-942-245-74	Sequence 74, Appl
272	5	10.2	1873	1	US-08-435-675B-4	Sequence 4, Appl	345	4	8.2	16	1	US-07-942-245-76	Sequence 76, Appl
273	5	10.2	1873	1	US-08-336-257A-7	Sequence 7, Appl	346	4	8.2	16	1	US-07-942-245-95	Sequence 95, Appl
274	4	8.2	4	1	US-07-694-983-5	Sequence 5, Appl	347	4	8.2	16	1	US-07-942-245-96	Sequence 96, Appl
275	4	8.2	5	1	US-07-945-982-4	Sequence 4, Appl	348	4	8.2	16	1	US-07-942-245-97	Sequence 97, Appl
276	4	8.2	5	1	US-08-372-455-4	Sequence 4, Appl	349	4	8.2	16	1	US-07-942-245-102	Sequence 102, App
277	4	8.2	6	1	US-08-056-200-27	Sequence 27, Appl	350	4	8.2	16	1	US-07-942-245-105	Sequence 105, App
278	4	8.2	6	1	US-08-056-200-80	Sequence 80, Appl	351	4	8.2	16	1	US-07-942-245-117	Sequence 117, App
279	4	8.2	6	2	US-08-800-644-27	Sequence 27, Appl	352	4	8.2	16	1	US-07-942-245-145	Sequence 145, App
280	4	8.2	6	2	US-08-800-644-80	Sequence 80, Appl	353	4	8.2	16	1	US-07-942-245-147	Sequence 147, App
281	4	8.2	6	4	US-08-875-309-9	Sequence 9, Appl	354	4	8.2	16	4	US-08-475-411A-6	Sequence 6, Appl
282	4	8.2	6	5	PCT-US96-00310-9	Sequence 9, Appl	355	4	8.2	16	4	US-08-875-309-16	Sequence 16, Appl
283	4	8.2	7	1	US-08-372-952-5	Sequence 5, Appl	356	4	8.2	16	4	US-09-171-705-24	Sequence 24, Appl
284	4	8.2	7	1	US-08-191-338A-6	Sequence 6, Appl	357	4	8.2	16	4	US-09-171-705-25	Sequence 25, Appl
285	4	8.2	7	4	US-08-875-309-5	Sequence 5, Appl	358	4	8.2	16	4	US-08-602-999A-203	Sequence 203, App
286	4	8.2	7	5	PCT-US96-00310-5	Sequence 5, Appl	359	4	8.2	16	4	US-08-478-029A-6	Sequence 6, Appl
287	4	8.2	7	6	5514590-12	Patent No. 5514590	360	4	8.2	16	5	PCT-US91-09422-28	Sequence 28, Appl
288	4	8.2	8	4	US-08-875-309-10	Sequence 10, Appl	361	4	8.2	16	5	PCT-US95-09261-4	Sequence 4, Appl
289	4	8.2	8	5	PCT-US96-00310-10	Sequence 10, Appl	362	4	8.2	16	6	5219837-1	Patent No. 5219837
290	4	8.2	9	1	US-08-097-830E-24	Sequence 24, Appl	363	4	8.2	17	1	US-07-794-288D-39	Sequence 39, Appl
291	4	8.2	9	2	US-08-456-112B-24	Sequence 24, Appl	364	4	8.2	17	3	US-07-963-538B-21	Sequence 21, Appl
292	4	8.2	9	6	5378464-12	Patent No. 5378464	365	4	8.2	17	3	US-08-331-625A-35	Sequence 35, Appl
293	4	8.2	10	2	US-08-556-597-153	Sequence 153, App	366	4	8.2	17	6	5219837-7	Patent No. 5219837
294	4	8.2	10	3	US-08-925-002-6	Sequence 6, Appl	367	4	8.2	17	6	5219837-9	Patent No. 5219837
295	4	8.2	10	6	5258287-42	Patent No. 5258287	368	4	8.2	18	1	US-07-794-288D-38	Sequence 38, Appl
296	4	8.2	11	1	US-07-666-719-18	Sequence 18, Appl	369	4	8.2	18	2	US-09-017-205-57	Sequence 57, Appl
297	4	8.2	11	4	US-09-224-785-26	Sequence 26, Appl	370	4	8.2	18	2	US-08-640-847C-29	Sequence 29, Appl
298	4	8.2	12	1	US-07-794-288D-44	Sequence 44, Appl	371	4	8.2	18	3	US-08-881-094-9	Sequence 9, Appl
299	4	8.2	12	1	US-08-260-562-66	Sequence 66, Appl	372	4	8.2	18	3	US-08-881-094-10	Sequence 10, Appl
300	4	8.2	12	5	PCT-US95-05471-66	Sequence 66, Appl	373	4	8.2	18	3	US-08-881-094-12	Sequence 12, Appl
301	4	8.2	13	1	US-07-781-254A-20	Sequence 20, Appl	374	4	8.2	18	6	5219837-2	Patent No. 5219837
302	4	8.2	13	1	US-07-794-288D-43	Sequence 43, Appl	375	4	8.2	18	6	5219837-3	Patent No. 5219837
303	4	8.2	13	1	US-08-520-599-4	Sequence 4, Appl	376	4	8.2	18	6	5219837-4	Patent No. 5219837
304	4	8.2	13	1	US-08-200-919-15	Sequence 15, Appl	377	4	8.2	18	6	5219837-5	Patent No. 5219837
305	4	8.2	13	3	US-09-188-579-29	Sequence 29, Appl	378	4	8.2	19	1	US-07-794-288D-37	Sequence 37, Appl
306	4	8.2	13	3	US-09-188-579-35	Sequence 35, Appl	379	4	8.2	19	1	US-07-794-288D-150	Sequence 150, App
307	4	8.2	14	1	US-07-794-288D-42	Sequence 42, Appl	380	4	8.2	19	2	US-08-248-839C-96	Sequence 96, Appl
308	4	8.2	14	2	US-07-963-538B-26	Sequence 26, Appl	381	4	8.2	19	2	US-09-174-060-14	Sequence 14, Appl
309	4	8.2	14	5	PCT-US95-13975-8	Sequence 8, Appl	382	4	8.2	19	3	US-08-338-382-14	Sequence 14, Appl
310	4	8.2	15	1	US-08-080-073-19	Sequence 19, Appl	383	4	8.2	19	3	US-08-467-023-236	Sequence 236, App
311	4	8.2	15	1	US-08-080-073-21	Sequence 21, Appl	384	4	8.2	19	4	US-08-652-877-18	Sequence 18, Appl
312	4	8.2	15	1	US-08-080-073-27	Sequence 27, Appl	385	4	8.2	19	5	PCT-US91-02942-67	Sequence 67, Appl
313	4	8.2	15	1	US-07-946-421-8	Sequence 8, Appl	386	4	8.2	20	1	US-08-205-938A-17	Sequence 17, Appl
314	4	8.2	15	1	US-07-794-288D-41	Sequence 41, Appl	387	4	8.2	20	1	US-07-794-288D-36	Sequence 36, Appl
315	4	8.2	15	1	US-08-423-399B-21	Sequence 21, Appl	388	4	8.2	20	1	US-07-794-288D-142	Sequence 142, App
316	4	8.2	15	1	US-08-582-257-13	Sequence 13, Appl	389	4	8.2	20	1	US-07-794-288D-149	Sequence 149, App
317	4	8.2	15	1	US-08-137-117D-121	Sequence 121, App	390	4	8.2	20	1	US-08-430-273-1	Sequence 1, Appl
318	4	8.2	14	1	US-08-137-117D-140	Sequence 140, App	391	4	8.2	20	1	US-07-678-974D-6	Sequence 6, Appl
319	4	8.2	15	1	US-08-434-705B-20	Sequence 20, Appl	392	4	8.2	20	1	US-07-678-974D-46	Sequence 46, Appl

393	4	8.2	20	2	US-08-480-190-35	Sequence 35, Appl	466	4	8.2	23	3	US-08-810-324-6	Sequence 6, Appl1
394	4	8.2	20	2	US-08-480-190-56	Sequence 56, Appl	467	4	8.2	23	3	US-08-810-324-31	Sequence 31, Appl
395	4	8.2	20	2	US-08-488-379-35	Sequence 35, Appl	468	4	8.2	23	3	US-08-810-324-34	Sequence 34, Appl
396	4	8.2	20	2	US-08-488-379-56	Sequence 56, Appl	469	4	8.2	24	1	US-08-103-445-21	Sequence 21, Appl
397	4	8.2	20	2	US-08-107-676-20	Sequence 20, Appl	470	4	8.2	24	1	US-07-794-288D-37	Sequence 37, Appl
398	4	8.2	20	2	US-08-107-676-21	Sequence 21, Appl	471	4	8.2	24	1	US-07-794-288D-72	Sequence 72, Appl
399	4	8.2	20	2	US-08-945-168-52	Sequence 52, Appl	472	4	8.2	24	1	US-07-794-288D-131	Sequence 131, App
400	4	8.2	20	3	US-08-788-231A-10	Sequence 10, Appl	473	4	8.2	24	1	US-07-794-288D-138	Sequence 138, App
401	4	8.2	20	5	PCT-US93-07545-35	Sequence 35, Appl	474	4	8.2	24	1	US-07-794-288D-145	Sequence 145, App
402	4	8.2	20	5	PCT-US93-07545-56	Sequence 56, Appl	475	4	8.2	24	1	US-08-325-071-30	Sequence 30, Appl
403	4	8.2	20	5	PCT-US95-02626-17	Sequence 17, Appl	476	4	8.2	24	1	US-08-461-690B-21	Sequence 21, Appl
404	4	8.2	21	1	US-07-666-719-8	Sequence 8, Appl1	477	4	8.2	24	1	US-08-244-701B-47	Sequence 47, Appl
405	4	8.2	21	1	US-07-918-953-15	Sequence 15, Appl	478	4	8.2	24	2	US-08-470-775-12	Sequence 12, Appl
406	4	8.2	21	1	US-08-212-696-1	Sequence 1, Appl1	479	4	8.2	24	3	US-09-054-393-5	Sequence 5, Appl1
407	4	8.2	21	1	US-08-158-245-1	Sequence 1, Appl1	480	4	8.2	24	3	US-08-469-318-51	Sequence 51, Appl
408	4	8.2	21	1	US-08-081-661-15	Sequence 15, Appl	481	4	8.2	24	3	US-08-468-609A-51	Sequence 51, Appl
409	4	8.2	21	1	US-08-233-617-1	Sequence 1, Appl1	482	4	8.2	24	3	US-08-192-325B-51	Sequence 51, Appl
410	4	8.2	21	1	US-08-160-376A-1	Sequence 1, Appl1	483	4	8.2	24	3	US-08-559-267A-12	Sequence 12, Appl
411	4	8.2	21	1	US-07-956-700B-18	Sequence 18, Appl	484	4	8.2	24	4	US-08-469-124-12	Sequence 34, Appl
412	4	8.2	21	1	US-08-304-070-1	Sequence 1, Appl1	485	4	8.2	24	4	US-08-847-844A-34	Sequence 34, Appl
413	4	8.2	21	1	US-08-285-661-1	Sequence 1, Appl1	486	4	8.2	24	5	PCT-US95-01185-51	Sequence 51, Appl
414	4	8.2	21	1	US-07-794-288D-35	Sequence 35, Appl	487	4	8.2	25	1	US-08-264-030-6	Sequence 6, Appl1
415	4	8.2	21	1	US-07-794-288D-134	Sequence 134, App	488	4	8.2	25	1	US-08-264-030-7	Sequence 7, Appl1
416	4	8.2	21	1	US-07-794-288D-141	Sequence 141, App	489	4	8.2	25	1	US-08-264-030-8	Sequence 8, Appl1
417	4	8.2	21	1	US-07-794-288D-148	Sequence 148, App	490	4	8.2	25	1	US-08-264-030-11	Sequence 11, Appl
418	4	8.2	21	1	US-08-301-838-1	Sequence 1, Appl1	491	4	8.2	25	1	US-07-794-288D-31	Sequence 31, Appl
419	4	8.2	21	1	US-08-447-925-3	Sequence 3, Appl1	492	4	8.2	25	1	US-07-794-288D-76	Sequence 76, Appl
420	4	8.2	21	1	US-08-389-487-4	Sequence 4, Appl1	493	4	8.2	25	1	US-07-794-288D-130	Sequence 130, App
421	4	8.2	21	1	US-08-389-487-12	Sequence 12, Appl	494	4	8.2	25	1	US-07-794-288D-137	Sequence 137, App
422	4	8.2	21	1	US-08-507-124-2	Sequence 2, Appl1	495	4	8.2	25	1	US-07-794-288D-144	Sequence 144, App
423	4	8.2	21	1	US-08-342-931-1	Sequence 1, Appl1	496	4	8.2	25	1	US-08-416-709-4	Sequence 4, Appl1
424	4	8.2	21	1	US-08-400-256-1	Sequence 1, Appl1	497	4	8.2	25	2	US-08-473-475A-13	Sequence 13, Appl
425	4	8.2	21	1	US-08-476-537-18	Sequence 18, Appl	498	4	8.2	25	4	US-08-974-549A-135	Sequence 135, App
426	4	8.2	21	1	US-08-485-607-18	Sequence 18, Appl	499	4	8.2	26	1	US-07-794-288D-30	Sequence 30, Appl
427	4	8.2	21	2	US-08-508-664-9	Sequence 9, Appl1	500	4	8.2	26	1	US-07-794-288D-75	Sequence 75, Appl
428	4	8.2	21	2	US-08-353-476-85	Sequence 85, Appl	501	4	8.2	26	1	US-07-794-288D-129	Sequence 129, App
429	4	8.2	21	2	US-08-484-219-1	Sequence 1, Appl1	502	4	8.2	26	1	US-07-794-288D-136	Sequence 136, App
430	4	8.2	21	2	US-08-979-587-1	Sequence 1, Appl1	503	4	8.2	26	1	US-07-794-288D-143	Sequence 143, App
431	4	8.2	21	2	US-08-475-879-18	Sequence 18, Appl	504	4	8.2	26	1	US-07-942-245-231	Sequence 231, App
432	4	8.2	21	2	US-08-992-676-6	Sequence 1, Appl1	505	4	8.2	26	1	US-07-942-245-232	Sequence 232, App
433	4	8.2	21	2	US-08-992-676-6	Sequence 6, Appl1	506	4	8.2	26	1	US-07-942-245-233	Sequence 233, App
434	4	8.2	21	2	US-09-134-836-1	Sequence 1, Appl1	507	4	8.2	26	1	US-07-942-245-234	Sequence 234, App
435	4	8.2	21	2	US-09-134-836-7	Sequence 7, Appl1	508	4	8.2	26	1	US-07-942-245-235	Sequence 235, App
436	4	8.2	21	3	US-08-967-867-2	Sequence 2, Appl1	509	4	8.2	26	1	US-07-942-245-236	Sequence 236, App
437	4	8.2	21	3	US-08-651-136C-44	Sequence 44, Appl	510	4	8.2	26	1	US-07-942-245-238	Sequence 238, App
438	4	8.2	21	3	US-08-975-365-1	Sequence 1, Appl1	511	4	8.2	26	1	US-07-942-245-239	Sequence 239, App
439	4	8.2	21	3	US-08-750-391-3	Sequence 3, Appl1	512	4	8.2	26	1	US-07-942-245-240	Sequence 240, App
440	4	8.2	21	3	US-08-788-231A-7	Sequence 7, Appl1	513	4	8.2	26	1	US-07-942-245-241	Sequence 241, App
441	4	8.2	21	6	5164366-3	Patent No. 5164366	514	4	8.2	26	1	US-07-942-245-242	Sequence 242, App
442	4	8.2	21	6	5164366-5	Patent No. 5164366	515	4	8.2	26	1	US-07-942-245-243	Sequence 243, App
443	4	8.2	21	6	5169865-4	Patent No. 5169865	516	4	8.2	26	1	US-07-942-245-248	Sequence 248, App
444	4	8.2	21	6	5514646-2	Patent No. 5514646	517	4	8.2	26	1	US-07-942-245-251	Sequence 251, App
445	4	8.2	21	6	5514646-50	Patent No. 5514646	518	4	8.2	26	1	US-07-942-245-252	Sequence 252, App
446	4	8.2	22	1	US-08-080-073-33	Sequence 33, Appl	519	4	8.2	26	1	US-07-942-245-258	Sequence 258, App
447	4	8.2	22	1	US-08-080-073-34	Sequence 34, Appl	520	4	8.2	26	1	US-07-942-245-261	Sequence 261, App
448	4	8.2	22	1	US-08-080-073-36	Sequence 36, Appl	521	4	8.2	26	1	US-07-942-245-269	Sequence 269, App
449	4	8.2	22	1	US-08-087-831-4	Sequence 4, Appl1	522	4	8.2	26	1	US-07-942-245-270	Sequence 270, App
450	4	8.2	22	1	US-07-794-288D-34	Sequence 34, Appl	523	4	8.2	26	1	US-07-942-245-285	Sequence 285, App
451	4	8.2	22	1	US-07-794-288D-79	Sequence 79, Appl	524	4	8.2	26	1	US-07-942-245-286	Sequence 286, App
452	4	8.2	22	1	US-07-794-288D-133	Sequence 133, App	525	4	8.2	26	1	US-07-942-245-287	Sequence 287, App
453	4	8.2	22	1	US-07-794-288D-140	Sequence 140, App	526	4	8.2	26	1	US-07-942-245-288	Sequence 288, App
454	4	8.2	22	1	US-07-794-288D-147	Sequence 147, App	527	4	8.2	26	1	US-07-942-245-290	Sequence 290, App
455	4	8.2	22	1	US-08-466-945-4	Sequence 4, Appl1	528	4	8.2	26	1	US-07-942-245-291	Sequence 291, App
456	4	8.2	22	2	US-08-248-839C-177	Patent No. 5204096	529	4	8.2	26	1	US-07-942-245-292	Sequence 292, App
457	4	8.2	22	6	5204096-8	Patent No. 5204096	530	4	8.2	26	1	US-07-942-245-293	Sequence 293, App
458	4	8.2	23	1	US-07-794-288D-33	Sequence 33, Appl	531	4	8.2	26	1	US-07-942-245-294	Sequence 294, App
459	4	8.2	23	1	US-07-794-288D-78	Sequence 78, Appl	532	4	8.2	26	1	US-07-942-245-295	Sequence 295, App
460	4	8.2	23	1	US-07-794-288D-132	Sequence 132, App	533	4	8.2	26	1	US-07-942-245-296	Sequence 296, App
461	4	8.2	23	1	US-07-794-288D-139	Sequence 139, App	534	4	8.2	26	1	US-07-942-245-297	Sequence 297, App
462	4	8.2	23	1	US-07-794-288D-146	Sequence 146, App	535	4	8.2	26	1	US-07-942-245-298	Sequence 298, App
463	4	8.2	23	3	US-08-746-160-10	Sequence 10, Appl	536	4	8.2	26	1	US-07-942-245-299	Sequence 299, App
464	4	8.2	23	3	US-08-746-160-35	Sequence 35, Appl	537	4	8.2	26	1	US-07-942-245-303	Sequence 303, App
465	4	8.2	23	3	US-08-746-160-38	Sequence 38, Appl	538	4	8.2	26	1	US-07-942-245-304	Sequence 304, App

539	4	8.2	26	1	US-07-942-245-305	Sequence 305, App	612	4	8.2	28	3	US-08-793-792-1	Sequence 1, Appl
540	4	8.2	26	1	US-07-942-245-306	Sequence 306, App	613	4	8.2	28	4	US-08-469-124-13	Sequence 13, Appl
541	4	8.2	26	1	US-07-942-245-312	Sequence 312, App	614	4	8.2	28	5	PCT-US95-01185-52	Sequence 52, Appl
542	4	8.2	26	1	US-07-942-245-315	Sequence 315, App	615	4	8.2	29	1	US-07-794-2880-27	Sequence 27, Appl
543	4	8.2	26	1	US-07-942-245-317	Sequence 317, App	616	4	8.2	29	1	US-07-794-2880-72	Sequence 72, Appl
544	4	8.2	26	1	US-07-942-245-323	Sequence 323, App	617	4	8.2	29	1	US-07-794-2880-94	Sequence 94, Appl
545	4	8.2	26	1	US-07-942-245-324	Sequence 324, App	618	4	8.2	29	1	US-07-794-2880-186	Sequence 186, App
546	4	8.2	26	1	US-07-942-245-325	Sequence 325, App	619	4	8.2	29	1	US-07-794-2880-187	Sequence 187, App
547	4	8.2	26	1	US-07-942-245-326	Sequence 326, App	620	4	8.2	29	1	US-07-794-2880-188	Sequence 188, App
548	4	8.2	26	1	US-07-942-245-327	Sequence 327, App	621	4	8.2	29	1	US-08-471-675A-1	Sequence 1, Appl
549	4	8.2	26	1	US-07-942-245-329	Sequence 329, App	622	4	8.2	30	1	US-07-946-421-11	Sequence 11, Appl
550	4	8.2	26	1	US-07-942-245-330	Sequence 330, App	623	4	8.2	30	1	US-07-794-2880-26	Sequence 26, Appl
551	4	8.2	26	1	US-07-942-245-331	Sequence 331, App	624	4	8.2	30	1	US-07-794-2880-178	Sequence 178, App
552	4	8.2	26	1	US-07-942-245-333	Sequence 333, App	625	4	8.2	30	1	US-07-794-2880-179	Sequence 179, App
553	4	8.2	26	1	US-07-942-245-337	Sequence 337, App	626	4	8.2	30	1	US-07-794-2880-180	Sequence 180, App
554	4	8.2	26	1	US-07-942-245-339	Sequence 339, App	627	4	8.2	30	1	US-07-794-2880-191	Sequence 191, App
555	4	8.2	26	1	US-07-942-245-340	Sequence 340, App	628	4	8.2	30	1	US-07-794-2880-192	Sequence 192, App
556	4	8.2	26	1	US-07-942-245-341	Sequence 341, App	629	4	8.2	30	1	US-07-794-2880-195	Sequence 195, App
557	4	8.2	26	1	US-07-942-245-342	Sequence 342, App	630	4	8.2	30	1	US-07-794-2880-218	Sequence 218, App
558	4	8.2	26	1	US-07-942-245-343	Sequence 343, App	631	4	8.2	30	1	US-07-794-2880-225	Sequence 225, App
559	4	8.2	26	1	US-07-942-245-345	Sequence 345, App	632	4	8.2	30	1	US-08-477-877B-52	Sequence 52, Appl
560	4	8.2	26	1	US-07-942-245-347	Sequence 347, App	633	4	8.2	30	1	US-08-262-037-30	Sequence 30, Appl
561	4	8.2	26	1	US-07-942-245-349	Sequence 349, App	634	4	8.2	30	1	US-08-244-701B-25	Sequence 25, Appl
562	4	8.2	26	1	US-07-942-245-350	Sequence 350, App	635	4	8.2	30	1	US-08-244-701B-26	Sequence 26, Appl
563	4	8.2	26	1	US-07-942-245-351	Sequence 351, App	636	4	8.2	30	1	US-08-137-117D-146	Sequence 146, App
564	4	8.2	26	1	US-07-942-245-353	Sequence 353, App	637	4	8.2	30	1	US-08-137-117D-152	Sequence 152, App
565	4	8.2	26	1	US-07-942-245-355	Sequence 355, App	638	4	8.2	30	1	US-08-137-117D-157	Sequence 157, App
566	4	8.2	26	1	US-07-942-245-356	Sequence 356, App	639	4	8.2	30	2	US-08-472-281A-52	Sequence 52, Appl
567	4	8.2	26	1	US-07-942-245-360	Sequence 360, App	640	4	8.2	30	2	US-08-436-717-146	Sequence 146, App
568	4	8.2	26	1	US-07-942-245-361	Sequence 361, App	641	4	8.2	30	2	US-08-436-717-152	Sequence 152, App
569	4	8.2	26	1	US-07-942-245-365	Sequence 365, App	642	4	8.2	30	2	US-08-436-717-157	Sequence 157, App
570	4	8.2	26	1	US-07-942-245-366	Sequence 366, App	643	4	8.2	30	2	US-08-560-558E-5	Sequence 5, Appl
571	4	8.2	26	1	US-07-942-245-367	Sequence 367, App	644	4	8.2	30	2	US-08-477-989B-52	Sequence 52, Appl
572	4	8.2	26	1	US-07-942-245-368	Sequence 368, App	645	4	8.2	30	4	US-08-649-100-18	Sequence 18, Appl
573	4	8.2	26	1	US-07-942-245-374	Sequence 374, App	646	4	8.2	30	4	US-08-649-100-34	Sequence 34, Appl
574	4	8.2	26	1	US-07-942-245-385	Sequence 385, App	647	4	8.2	30	4	US-08-569-147-54	Sequence 54, Appl
575	4	8.2	26	1	US-07-942-245-458	Sequence 458, App	648	4	8.2	30	4	US-08-569-147-55	Sequence 55, Appl
576	4	8.2	26	1	US-07-942-245-459	Sequence 459, App	649	4	8.2	31	1	US-07-776-272-23	Sequence 23, Appl
577	4	8.2	26	1	US-07-942-245-460	Sequence 460, App	650	4	8.2	31	1	US-08-244-701B-31	Sequence 31, Appl
578	4	8.2	26	1	US-07-942-245-461	Sequence 461, App	651	4	8.2	32	3	US-08-665-259-17	Sequence 17, Appl
579	4	8.2	26	1	US-07-942-245-462	Sequence 462, App	652	4	8.2	32	3	US-08-762-500-17	Sequence 17, Appl
580	4	8.2	26	1	US-07-942-245-463	Sequence 463, App	653	4	8.2	32	3	US-08-793-792-5	Sequence 5, Appl
581	4	8.2	26	1	US-07-942-245-466	Sequence 466, App	654	4	8.2	32	4	US-08-513-968-55	Sequence 55, Appl
582	4	8.2	26	1	US-07-942-245-467	Sequence 467, App	655	4	8.2	33	3	US-08-469-318-191	Sequence 191, App
583	4	8.2	26	1	US-08-487-890A-72	Sequence 72, Appl	656	4	8.2	33	3	US-08-469-318-192	Sequence 192, App
584	4	8.2	26	2	US-08-478-435-72	Sequence 72, Appl	657	4	8.2	33	3	US-08-469-318-193	Sequence 193, App
585	4	8.2	26	2	US-08-337-483-72	Sequence 72, Appl	658	4	8.2	33	3	US-08-468-609A-191	Sequence 191, App
586	4	8.2	26	2	US-08-478-373-72	Sequence 72, Appl	659	4	8.2	33	3	US-08-468-609A-192	Sequence 192, App
587	4	8.2	26	2	US-08-620-151-14	Sequence 14, Appl	660	4	8.2	33	3	US-08-468-609A-193	Sequence 193, App
588	4	8.2	26	3	US-08-474-671-72	Sequence 72, Appl	661	4	8.2	33	5	PCT-US95-01185-191	Sequence 191, App
589	4	8.2	26	3	US-08-483-577A-72	Sequence 72, Appl	662	4	8.2	33	5	PCT-US95-01185-192	Sequence 192, App
590	4	8.2	26	4	US-08-974-549A-57	Sequence 57, Appl	663	4	8.2	33	5	PCT-US95-01185-193	Sequence 193, App
591	4	8.2	27	1	US-08-066-277-1	Sequence 1, Appl	664	4	8.2	35	1	US-08-487-890A-55	Sequence 55, Appl
592	4	8.2	27	1	US-07-794-2880-29	Sequence 29, Appl	665	4	8.2	35	2	US-08-392-625-35	Sequence 35, Appl
593	4	8.2	27	1	US-07-794-2880-74	Sequence 74, Appl	666	4	8.2	35	2	US-08-466-961A-35	Sequence 35, Appl
594	4	8.2	27	1	US-07-942-2880-128	Sequence 128, App	667	4	8.2	35	2	US-08-478-435-55	Sequence 55, Appl
595	4	8.2	27	1	US-07-794-2880-135	Sequence 135, App	668	4	8.2	35	2	US-08-337-483-55	Sequence 55, Appl
596	4	8.2	27	1	US-08-550-815-1	Sequence 1, Appl	669	4	8.2	35	2	US-08-478-373-55	Sequence 55, Appl
597	4	8.2	27	3	US-08-703-089-1	Sequence 1, Appl	670	4	8.2	35	2	US-08-460-890A-45	Sequence 45, Appl
598	4	8.2	28	1	US-08-264-030-2	Sequence 2, Appl	671	4	8.2	35	3	US-08-474-671-55	Sequence 55, Appl
599	4	8.2	28	1	US-08-264-030-3	Sequence 3, Appl	672	4	8.2	35	3	US-08-483-577A-55	Sequence 55, Appl
600	4	8.2	28	1	US-08-264-030-4	Sequence 4, Appl	673	4	8.2	35	3	US-08-167-641C-45	Sequence 45, Appl
601	4	8.2	28	1	US-08-264-030-5	Sequence 5, Appl	674	4	8.2	35	4	US-08-460-971A-45	Sequence 45, Appl
602	4	8.2	28	1	US-08-264-030-10	Sequence 10, Appl	675	4	8.2	35	4	US-08-462-040-45	Sequence 45, Appl
603	4	8.2	28	1	US-07-794-2880-28	Sequence 28, Appl	676	4	8.2	36	1	US-07-882-923-1	Sequence 1, Appl
604	4	8.2	28	1	US-07-794-2880-73	Sequence 73, Appl	677	4	8.2	36	1	US-07-882-923-2	Sequence 2, Appl
605	4	8.2	28	1	US-07-794-2880-127	Sequence 127, App	678	4	8.2	36	1	US-08-264-030-1	Sequence 1, Appl
606	4	8.2	28	2	US-08-470-775-13	Sequence 13, Appl	679	4	8.2	36	1	US-08-338-395-3	Sequence 3, Appl
607	4	8.2	28	2	US-08-859-106A-8	Sequence 8, Appl	680	4	8.2	36	1	US-08-338-395-4	Sequence 4, Appl
608	4	8.2	28	3	US-08-469-318-52	Sequence 52, Appl	681	4	8.2	36	1	US-08-329-151-24	Sequence 24, Appl
609	4	8.2	28	3	US-08-468-609A-52	Sequence 52, Appl	682	4	8.2	36	1	US-08-487-890A-37	Sequence 37, Appl
610	4	8.2	28	3	US-08-152-325B-52	Sequence 52, Appl	683	4	8.2	36	2	US-08-478-435-37	Sequence 37, Appl
611	4	8.2	28	3	US-08-559-267A-13	Sequence 13, Appl	684	4	8.2	36	2	US-08-337-483-37	Sequence 37, Appl

685	4	8.2	36	2	US-08-478-373-37	Sequence 37, Appl	758	4	8.2	49	1	US-07-662-225A-3	Sequence 3, Appl
686	4	8.2	36	3	US-08-474-671-37	Sequence 37, Appl	759	4	8.2	49	1	US-07-602-847C-22	Sequence 22, Appl
687	4	8.2	36	3	US-08-907-403A-1	Sequence 1, Appl	760	4	8.2	49	1	US-07-965-674-6	Sequence 6, Appl
688	4	8.2	36	3	US-08-907-403A-2	Sequence 2, Appl	761	4	8.2	49	1	US-08-304-051-1	Sequence 1, Appl
689	4	8.2	36	3	US-08-483-577A-37	Sequence 37, Appl	762	4	8.2	49	1	US-08-478-039-87	Sequence 87, Appl
690	4	8.2	36	5	PCT-US95-14303-3	Sequence 3, Appl	763	4	8.2	49	1	US-08-476-349A-87	Sequence 87, Appl
691	4	8.2	36	5	PCT-US95-14303-4	Sequence 4, Appl	764	4	8.2	49	3	US-07-963-538B-3	Sequence 3, Appl
692	4	8.2	37	1	US-07-794-288D-3	Sequence 3, Appl	765	4	8.2	49	3	US-08-995-156A-27	Sequence 27, Appl
693	4	8.2	37	1	US-08-233-389C-8	Sequence 8, Appl	766	4	8.2	49	3	US-08-995-156A-72	Sequence 72, Appl
694	4	8.2	37	1	US-08-233-389C-9	Sequence 9, Appl	767	4	8.2	49	5	PCT-US93-05640-21	Sequence 21, Appl
695	4	8.2	37	2	US-08-801-863-8	Sequence 8, Appl	768	4	8.2	49	5	PCT-US93-05640-6	Sequence 6, Appl
696	4	8.2	37	2	US-08-801-863-9	Sequence 9, Appl	769	4	8.2	49	5	PCT-US93-05640-11	Sequence 11, Appl
697	4	8.2	37	2	US-08-486-586A-8	Sequence 8, Appl	770	4	8.2	50	1	PCT-US95-11445-1	Sequence 32, Appl
698	4	8.2	37	2	US-08-486-586A-9	Sequence 9, Appl	771	4	8.2	50	2	US-07-963-538B-2	Sequence 2, Appl
699	4	8.2	37	2	US-09-004-713-8	Sequence 8, Appl	772	4	8.2	50	3	US-08-995-156A-28	Sequence 28, Appl
700	4	8.2	37	2	US-09-004-713-9	Sequence 9, Appl	773	4	8.2	50	3	US-08-995-156A-73	Sequence 73, Appl
701	4	8.2	37	2	US-08-619-841-1	Sequence 1, Appl	774	4	8.2	50	5	PCT-US91-02942-6	Sequence 6, Appl
702	4	8.2	37	2	US-08-619-841-2	Sequence 2, Appl	775	4	8.2	50	5	PCT-US91-02942-7	Sequence 7, Appl
703	4	8.2	37	2	US-08-446-929A-1	Sequence 1, Appl	776	4	8.2	50	5	PCT-US91-02942-46	Sequence 46, Appl
704	4	8.2	37	2	US-08-446-929A-2	Sequence 2, Appl	777	4	8.2	50	5	PCT-US91-02942-47	Sequence 47, Appl
705	4	8.2	37	3	US-08-793-792-9	Sequence 9, Appl	778	4	8.2	50	5	PCT-US91-02942-48	Sequence 48, Appl
706	4	8.2	37	6	5424221-4	Patent No. 5424221	779	4	8.2	50	5	PCT-US91-02942-49	Sequence 49, Appl
707	4	8.2	37	6	5424221-5	Patent No. 5424221	780	4	8.2	50	5	PCT-US91-02942-50	Sequence 50, Appl
708	4	8.2	38	1	US-07-776-272-19	Sequence 19, Appl	781	4	8.2	51	1	US-07-707-542E-1	Sequence 1, Appl
709	4	8.2	38	1	US-07-776-272-20	Sequence 20, Appl	782	4	8.2	51	1	US-07-707-542E-2	Sequence 2, Appl
710	4	8.2	38	1	US-07-776-272-21	Sequence 21, Appl	783	4	8.2	51	1	US-07-707-542E-4	Sequence 4, Appl
711	4	8.2	38	1	US-07-776-272-22	Sequence 22, Appl	784	4	8.2	51	1	US-07-707-542E-5	Sequence 5, Appl
712	4	8.2	38	2	US-08-448-8141-9	Sequence 9, Appl	785	4	8.2	51	1	US-07-945-982-1	Sequence 1, Appl
713	4	8.2	38	2	US-08-460-890A-44	Sequence 44, Appl	786	4	8.2	51	1	US-08-372-455-1	Sequence 1, Appl
714	4	8.2	38	3	US-08-167-641C-44	Sequence 44, Appl	787	4	8.2	51	1	US-08-082-842A-73	Sequence 73, Appl
715	4	8.2	38	4	US-08-460-971A-44	Sequence 44, Appl	788	4	8.2	51	1	US-08-082-842A-74	Sequence 74, Appl
716	4	8.2	38	4	US-08-462-040-44	Sequence 44, Appl	789	4	8.2	51	1	US-08-082-842A-75	Sequence 75, Appl
717	4	8.2	39	1	US-07-662-225A-4	Sequence 4, Appl	790	4	8.2	51	1	US-08-472-788A-74	Sequence 74, Appl
718	4	8.2	39	1	US-07-662-225A-5	Sequence 5, Appl	791	4	8.2	51	1	US-08-812-025-3	Sequence 3, Appl
719	4	8.2	39	1	US-08-212-236-3	Sequence 3, Appl	792	4	8.2	51	2	US-08-082-842A-73	Sequence 73, Appl
720	4	8.2	39	1	US-08-212-236-4	Sequence 4, Appl	793	4	8.2	51	2	US-08-082-842A-74	Sequence 74, Appl
721	4	8.2	39	3	US-08-258-287B-46	Sequence 46, Appl	794	4	8.2	51	2	US-08-761-248B-14	Sequence 14, Appl
722	4	8.2	39	3	US-08-368-704C-45	Sequence 45, Appl	795	4	8.2	51	2	US-08-800-644-113	Sequence 113, Appl
723	4	8.2	40	1	US-07-666-719-3	Sequence 3, Appl	796	4	8.2	51	3	US-08-995-156A-29	Sequence 29, Appl
724	4	8.2	40	1	US-08-262-037-31	Sequence 31, Appl	797	4	8.2	51	3	US-08-995-156A-74	Sequence 74, Appl
725	4	8.2	40	1	US-08-645-193B-66	Sequence 66, Appl	798	4	8.2	52	1	US-07-745-206A-28	Sequence 28, Appl
726	4	8.2	40	3	US-08-812-586-39	Sequence 39, Appl	799	4	8.2	52	2	US-08-311-363-28	Sequence 28, Appl
727	4	8.2	40	3	US-08-812-586-40	Sequence 40, Appl	800	4	8.2	52	2	US-08-995-156A-30	Sequence 30, Appl
728	4	8.2	40	3	US-08-477-383-56	Sequence 56, Appl	801	4	8.2	52	3	US-08-995-156A-75	Sequence 75, Appl
729	4	8.2	41	1	US-08-487-174-56	Sequence 56, Appl	802	4	8.2	53	1	US-08-233-617-3	Sequence 3, Appl
730	4	8.2	42	1	US-08-447-925-2	Sequence 2, Appl	803	4	8.2	53	1	US-08-233-617-4	Sequence 4, Appl
731	4	8.2	42	1	US-08-480-750-56	Sequence 56, Appl	804	4	8.2	53	1	US-08-290-919-3	Sequence 3, Appl
732	4	8.2	42	1	US-08-520-599-1	Sequence 1, Appl	805	4	8.2	53	1	US-08-290-919-4	Sequence 4, Appl
733	4	8.2	42	1	US-08-099-334-8	Sequence 8, Appl	806	4	8.2	53	2	US-07-963-538B-1	Sequence 1, Appl
734	4	8.2	42	2	US-08-288-059-34	Sequence 34, Appl	807	4	8.2	53	3	US-08-651-136C-48	Sequence 48, Appl
735	4	8.2	43	2	US-08-499-676A-33	Sequence 33, Appl	808	4	8.2	53	3	US-08-995-156A-31	Sequence 31, Appl
736	4	8.2	44	2	US-08-437-607A-47	Sequence 47, Appl	809	4	8.2	53	3	US-08-995-156A-76	Sequence 76, Appl
737	4	8.2	44	2	US-08-761-248B-8	Sequence 8, Appl	810	4	8.2	53	4	US-09-261-853-2	Sequence 2, Appl
738	4	8.2	45	3	US-08-856-074A-29	Sequence 29, Appl	811	4	8.2	54	3	US-08-995-156A-32	Sequence 32, Appl
739	4	8.2	45	3	US-08-995-156A-23	Sequence 23, Appl	812	4	8.2	54	3	US-08-995-156A-77	Sequence 77, Appl
740	4	8.2	46	2	US-08-511-485-35	Sequence 35, Appl	813	4	8.2	55	1	US-08-262-037-118	Sequence 118, Appl
741	4	8.2	46	2	US-08-511-485-37	Sequence 37, Appl	814	4	8.2	55	2	US-08-437-607A-49	Sequence 49, Appl
742	4	8.2	46	2	US-08-511-485-38	Sequence 38, Appl	815	4	8.2	55	3	US-08-995-156A-33	Sequence 33, Appl
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744	4	8.2	46	3	US-08-995-156A-24	Sequence 24, Appl	817	4	8.2	56	1	US-08-160-376A-7	Sequence 7, Appl
745	4	8.2	46	3	US-08-995-156A-69	Sequence 69, Appl	818	4	8.2	56	1	US-08-389-487-11	Sequence 11, Appl
746	4	8.2	47	1	US-08-331-394-6	Sequence 6, Appl	819	4	8.2	56	1	US-08-556-823-1	Sequence 1, Appl
747	4	8.2	47	1	US-08-250-858-6	Sequence 6, Appl	820	4	8.2	56	1	US-08-556-823-9	Sequence 9, Appl
748	4	8.2	47	1	US-08-446-915-6	Sequence 6, Appl	821	4	8.2	56	3	US-08-995-156A-34	Sequence 34, Appl
749	4	8.2	47	2	US-08-248-839C-52	Sequence 52, Appl	822	4	8.2	56	3	US-08-995-156A-79	Sequence 79, Appl
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751	4	8.2	47	3	US-08-995-156A-25	Sequence 25, Appl	824	4	8.2	56	6	5217896-7	Patent No. 5217896
752	4	8.2	47	3	US-08-995-156A-70	Sequence 70, Appl	825	4	8.2	57	1	US-08-030-731A-44	Sequence 44, Appl
753	4	8.2	47	5	PCT-US95-06639-6	Sequence 6, Appl	826	4	8.2	57	3	US-08-995-156A-35	Sequence 35, Appl
754	4	8.2	48	3	US-08-995-156A-26	Sequence 26, Appl	827	4	8.2	57	3	US-08-995-156A-80	Sequence 80, Appl
755	4	8.2	48	3	US-08-995-156A-71	Sequence 71, Appl	828	4	8.2	58	3	US-08-995-156A-36	Sequence 36, Appl
756	4	8.2	49	1	US-07-662-225A-1	Sequence 1, Appl	829	4	8.2	58	3	US-08-995-156A-81	Sequence 81, Appl
757	4	8.2	49	1	US-07-662-225A-2	Sequence 2, Appl	830	4	8.2	59	3	US-08-995-156A-37	Sequence 37, Appl

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833	4	8.2	60	1	US-08-447-9251-1	Sequence 1, Appl	906	4	8.2	74	5	PCT-US95-02275-21	Sequence 2, Appl
834	4	8.2	60	1	US-08-099-354-7	Sequence 7, Appl	907	4	8.2	75	3	US-08-995-156A-53	Sequence 53, Appl
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836	4	8.2	60	2	US-08-288-059-33	Sequence 33, Appl	909	4	8.2	76	2	US-08-356-361-28	Sequence 28, Appl
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838	4	8.2	60	2	US-08-706-270A-10	Sequence 10, Appl	911	4	8.2	76	3	US-08-995-156A-54	Sequence 54, Appl
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841	4	8.2	60	2	US-08-968-542C-14	Sequence 14, Appl	914	4	8.2	77	3	US-08-995-156A-55	Sequence 55, Appl
842	4	8.2	60	3	US-08-651-136C-70	Sequence 70, Appl	915	4	8.2	77	3	US-08-995-156A-100	Sequence 100, Appl
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844	4	8.2	60	3	US-08-483-503A-3	Sequence 3, Appl	917	4	8.2	78	2	US-08-467-123B-6	Sequence 6, Appl
845	4	8.2	60	3	US-08-995-156A-38	Sequence 38, Appl	918	4	8.2	78	3	US-08-995-156A-56	Sequence 56, Appl
846	4	8.2	60	3	US-08-995-156A-83	Sequence 83, Appl	919	4	8.2	78	3	US-08-995-156A-101	Sequence 101, Appl
847	4	8.2	61	1	US-08-262-037-33	Sequence 33, Appl	920	4	8.2	79	1	US-08-665-220-65	Sequence 65, Appl
848	4	8.2	61	2	US-08-744-670-6	Sequence 6, Appl	921	4	8.2	79	2	US-08-499-676A-14	Sequence 14, Appl
849	4	8.2	61	2	US-09-149-933-6	Sequence 6, Appl	922	4	8.2	79	3	US-08-995-156A-57	Sequence 57, Appl
850	4	8.2	61	3	US-08-995-156A-39	Sequence 39, Appl	923	4	8.2	79	3	US-08-995-156A-102	Sequence 102, Appl
851	4	8.2	61	3	US-08-995-156A-84	Sequence 84, Appl	924	4	8.2	80	1	US-08-137-800-41	Sequence 41, Appl
852	4	8.2	62	1	US-08-383-761-11	Sequence 11, Appl	925	4	8.2	80	1	US-08-477-383-41	Sequence 41, Appl
853	4	8.2	62	1	US-08-702-080-5	Sequence 5, Appl	926	4	8.2	80	1	US-08-487-174-41	Sequence 41, Appl
854	4	8.2	62	1	US-08-824-277-11	Sequence 11, Appl	927	4	8.2	80	1	US-08-480-750-41	Sequence 41, Appl
855	4	8.2	62	1	US-08-556-823-8	Sequence 8, Appl	928	4	8.2	80	2	US-08-553-501A-85	Sequence 85, Appl
856	4	8.2	62	2	US-08-913-050A-8	Sequence 8, Appl	929	4	8.2	80	2	US-08-765-783A-104	Sequence 104, Appl
857	4	8.2	62	2	US-08-858-830-5	Sequence 5, Appl	930	4	8.2	80	3	US-08-554-840-12	Sequence 12, Appl
858	4	8.2	62	2	US-08-858-834-5	Sequence 5, Appl	931	4	8.2	80	3	US-08-995-156A-58	Sequence 58, Appl
859	4	8.2	62	3	US-08-995-156A-40	Sequence 40, Appl	932	4	8.2	80	3	US-08-995-156A-103	Sequence 103, Appl
860	4	8.2	62	3	US-08-995-156A-85	Sequence 85, Appl	933	4	8.2	80	4	US-09-203-231-85	Sequence 85, Appl
861	4	8.2	63	1	US-08-160-376A-6	Sequence 6, Appl	934	4	8.2	81	3	US-08-995-156A-59	Sequence 59, Appl
862	4	8.2	63	1	US-08-372-723-1	Sequence 1, Appl	935	4	8.2	81	3	US-08-995-156A-104	Sequence 104, Appl
863	4	8.2	63	3	US-08-995-156A-41	Sequence 41, Appl	936	4	8.2	82	1	US-08-497-312-30	Sequence 30, Appl
864	4	8.2	63	3	US-08-995-156A-86	Sequence 86, Appl	937	4	8.2	82	3	US-08-995-156A-60	Sequence 60, Appl
865	4	8.2	64	1	US-08-372-723-2	Sequence 2, Appl	938	4	8.2	82	3	US-08-995-156A-105	Sequence 105, Appl
866	4	8.2	64	2	US-08-765-179B-10	Sequence 10, Appl	939	4	8.2	83	2	US-08-726-306A-76	Sequence 76, Appl
867	4	8.2	64	3	US-08-995-156A-42	Sequence 42, Appl	940	4	8.2	83	3	US-08-995-156A-61	Sequence 61, Appl
868	4	8.2	64	3	US-08-995-156A-87	Sequence 87, Appl	941	4	8.2	83	3	US-08-995-156A-106	Sequence 106, Appl
869	4	8.2	65	1	US-08-468-674B-71	Sequence 71, Appl	942	4	8.2	83	3	US-08-875-811-2	Sequence 2, Appl
870	4	8.2	65	1	US-08-780-571-71	Sequence 71, Appl	943	4	8.2	83	4	US-07-791-931-3	Sequence 3, Appl
871	4	8.2	65	3	US-08-995-156A-43	Sequence 43, Appl	944	4	8.2	84	3	US-08-995-156A-62	Sequence 62, Appl
872	4	8.2	65	3	US-08-995-156A-88	Sequence 88, Appl	945	4	8.2	84	3	US-08-995-156A-107	Sequence 107, Appl
873	4	8.2	65	5	PCT-US91-01840-7	Sequence 7, Appl	946	4	8.2	85	3	US-08-995-156A-63	Sequence 63, Appl
874	4	8.2	66	1	US-08-291-060B-5	Sequence 5, Appl	947	4	8.2	85	3	US-08-995-156A-108	Sequence 108, Appl
875	4	8.2	66	3	US-08-995-156A-44	Sequence 44, Appl	948	4	8.2	86	1	US-07-715-183C-1	Sequence 1, Appl
876	4	8.2	66	3	US-08-995-156A-89	Sequence 89, Appl	949	4	8.2	86	1	US-08-497-312-27	Sequence 27, Appl
877	4	8.2	67	3	US-08-995-156A-45	Sequence 45, Appl	950	4	8.2	86	2	US-08-465-380-45	Sequence 45, Appl
878	4	8.2	67	3	US-08-995-156A-90	Sequence 90, Appl	951	4	8.2	86	2	US-08-465-380-46	Sequence 46, Appl
879	4	8.2	68	3	US-08-995-156A-46	Sequence 46, Appl	952	4	8.2	86	2	US-08-486-397-45	Sequence 45, Appl
880	4	8.2	68	3	US-08-995-156A-91	Sequence 91, Appl	953	4	8.2	86	2	US-08-486-397-46	Sequence 46, Appl
881	4	8.2	68	3	US-08-912-272-19	Sequence 19, Appl	954	4	8.2	86	2	US-08-486-399-45	Sequence 45, Appl
882	4	8.2	68	3	US-08-912-272-23	Sequence 23, Appl	955	4	8.2	86	2	US-08-486-399-46	Sequence 46, Appl
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887	4	8.2	69	3	US-08-995-156A-92	Sequence 92, Appl	960	4	8.2	86	3	US-08-995-156A-64	Sequence 64, Appl
888	4	8.2	69	5	PCT-US95-02275-17	Sequence 17, Appl	961	4	8.2	86	3	US-08-995-156A-109	Sequence 109, Appl
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891	4	8.2	70	3	US-08-995-156A-93	Sequence 93, Appl	964	4	8.2	86	3	US-09-249-472-45	Sequence 45, Appl
892	4	8.2	71	3	US-08-995-156A-49	Sequence 49, Appl	965	4	8.2	86	3	US-09-249-472-46	Sequence 46, Appl
893	4	8.2	71	3	US-08-995-156A-94	Sequence 94, Appl	966	4	8.2	86	3	US-09-249-451-45	Sequence 45, Appl
894	4	8.2	72	3	US-08-995-156A-95	Sequence 50, Appl	967	4	8.2	86	3	US-09-249-451-46	Sequence 46, Appl
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897	4	8.2	73	3	US-08-995-156A-96	Sequence 96, Appl	970	4	8.2	86	3	US-09-249-461-45	Sequence 45, Appl
898	4	8.2	74	1	US-08-543-238-2	Sequence 2, Appl	971	4	8.2	86	3	US-09-249-461-46	Sequence 46, Appl
899	4	8.2	74	1	US-08-420-526-2	Sequence 2, Appl	972	4	8.2	86	4	US-09-249-448-45	Sequence 45, Appl
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901	4	8.2	74	1	US-08-457-459-21	Sequence 21, Appl	974	4	8.2	87	1	US-08-497-312-16	Sequence 16, Appl
902	4	8.2	74	1	US-08-555-678-21	Sequence 21, Appl	975	4	8.2	87	2	US-08-463-380-44	Sequence 44, Appl
903	4	8.2	74	3	US-08-995-156A-52	Sequence 52, Appl	976	4	8.2	87	2	US-08-486-397-44	Sequence 44, Appl

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980 4 8.2 87 3 US-08-995-156A-65 Sequence 65, Appl  
981 4 8.2 87 3 US-08-995-156A-110 Sequence 110, Appl  
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## ALIGNMENTS

RESULT 1  
5194595-19  
; Patent No. 5194595  
; APPLICANT: WATHEN, MICHAEL W.  
; TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING  
; IMMUNOGENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY  
; SYNCYTIAL VIRUS

; NUMBER OF SEQUENCES: 19  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/543,780  
; FILING DATE: 31-OCT-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 137,387  
; FILING DATE: 23-DEC-1987  
; SEQ ID NO:19:  
; LENGTH: 681  
5194595-19

Query Match 100.0%; Score 49; DB 6; Length 681;  
Best Local Similarity 100.0%; Pred. No. 6.3e-43;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNDFHFEVFNPCSCSNNTCWAICKRIPNKKPGKK 49  
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Db 543 KORONKPPSKPNDFHFEVFNPCSCSNNTCWAICKRIPNKKPGKK 591  
|||||

RESULT 2  
US-08-467-963C-8  
; Sequence 8, Application US/08467963C  
; Patent No. 5968776  
; GENERAL INFORMATION:  
; APPLICANT: KLEIN, Michel H  
; APPLICANT: DU, Run-Pan  
; APPLICANT: EWASYSHYN, Mary E  
; TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A  
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST  
; TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto

; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,963C  
; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/838,189  
; FILING DATE: 16-APR-1997  
; APPLICATION NUMBER: US 08/001,554  
; FILING DATE: 06-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9200117.1  
; FILING DATE: 06-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEWART, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-474 MIS:jb  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 298 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-467-963C-8

Query Match 81.6%; Score 40; DB 2; Length 298;  
Best Local Similarity 100.0%; Pred. No. 5.6e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDFHFEVFNPCSCSNNTCWAICKRIPNKKPGKK 49  
|||||  
Db 158 KPNDFHFEVFNPCSCSNNTCWAICKRIPNKKPGKK 197  
|||||

RESULT 3  
US-08-838-189D-8  
; Sequence 8, Application US/08838189D  
; Patent No. 5998169  
; GENERAL INFORMATION:  
; APPLICANT: KLEIN, Michel H  
; APPLICANT: DU, Run-Pan  
; APPLICANT: EWASYSHYN, Mary E  
; TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A  
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST  
; TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,189D  
; FILING DATE: 16-APR-1997  
; CLASSIFICATION: 435

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; SEQUENCE CHARACTERISTICS:  
; LENGTH: 298 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-852-344D-8  
  
Query Match      81.6%; Score 40; DB 3; Length 298;  
Best Local Similarity 100.0%; Pred. No. 5.6e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY    10 KPNNDFFHFVFNFPVCISNNPTCWAICKRIPNKKPKGK 49  
      |  
Db     158 KPNNDFFHFVFNFPVCISNNPTCWAICKRIPNKKPKGK 197  
  
RESULT          5  
US-08-344-639E-8  
; Sequence 8, Application US/08344639E  
; Patent No. 6033668  
; GENERAL INFORMATION:  
; APPLICANT: Klein, Michel H  
; APPLICANT: Du, Run-Pan  
; APPLICANT: Emwasyhyn, Mary E  
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS  
; TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS  
; TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 330 University Avenue, 6th Floor  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/344,639E  
; FILING DATE: 14-NOV-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/001,554  
; FILING DATE: 06-JAN-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9200117.1  
; FILING DATE: 06-JAN-1992  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-391 MIS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; TELEX: 065-24567 SIMBAS  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 298 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-344-639E-8  
  
Query Match      81.6%; Score 40; DB 3; Length 298;  
Best Local Similarity 100.0%; Pred. No. 5.6e-34;
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; FILING DATE:  
; CLASSIFICATION: 514  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-793-792-12

Query Match 73.5%; Score 36; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e-30;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNDHFHEVFVPCISCSNNPTCWAICKRIPNKK 45  
Db 2 KPNDHFHEVFVPCISCSNNPTCWAICKRIPNKK 37

RESULT 9  
US-08-792-8  
; Sequence 8, Application US/08793792  
; Patent No. 6077511  
; GENERAL INFORMATION:

; APPLICANT:  
; TITLE OF INVENTION: Antigenic peptides derived from the  
; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis  
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.  
; NUMBER OF SEQUENCES: 13  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION NUMBER: US/08/793,792  
; FILING DATE:

; CLASSIFICATION: 514  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-793-792-8

Query Match 65.3%; Score 32; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.5e-26;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNDHFHEVFVPCISCSNNPTCWAICKRI 41  
Db 1 KPNDHFHEVFVPCISCSNNPTCWAICKRI 32

RESULT 10  
US-08-793-792-4  
; Sequence 4, Application US/08793792  
; Patent No. 6077511  
; GENERAL INFORMATION:

; APPLICANT:  
; TITLE OF INVENTION: Antigenic peptides derived from the  
; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis  
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.  
; NUMBER OF SEQUENCES: 13  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,792  
; FILING DATE:

; CLASSIFICATION: 514  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-793-792-4

Query Match 57.1%; Score 28; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.7e-22;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PNNDHFHEVFVPCISCSNNPTCWAIC 38  
Db 1 PNNDHFHEVFVPCISCSNNPTCWAIC 28

RESULT 11  
US-08-793-792-13  
; Sequence 13, Application US/08793792  
; Patent No. 6077511  
; GENERAL INFORMATION:

; APPLICANT:  
; TITLE OF INVENTION: Antigenic peptides derived from the  
; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis  
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.  
; NUMBER OF SEQUENCES: 13  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/793,792  
; FILING DATE:  
; CLASSIFICATION: 514  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-793-792-13

Query Match 32.7%; Score 16; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.2e-10;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 SICSNPTCWAICKRI 41  
Db 1 SICSNPTCWAICKRI 16

RESULT 12  
US-08-793-792-3  
; Sequence 3, Application US/08793792  
; Patent No. 6077511  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Antigenic peptides derived from the

;; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis  
;; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.  
;; NUMBER OF SEQUENCES: 13  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/793,792  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 28 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
US-08-793-792-3

Query Match 26.5%; Score 13; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 4.2e-07;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HFEVFNVPSCIC 28  
| | | | | | | | | |  
Db 6 HFEVFNVPSCIC 18

RESULT 13  
US-08-793-792-7  
;; Sequence 7, Application US/08793792  
;; Patent No. 6077511  
;; GENERAL INFORMATION:  
;; APPLICANT:  
;; TITLE OF INVENTION: Antigenic peptides derived from the  
;; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis  
;; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.  
;; NUMBER OF SEQUENCES: 13  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/793,792  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 32 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
US-08-793-792-7

Query Match 26.5%; Score 13; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.6e-07;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HFEVFNVPSCIC 28  
| | | | | | | | | |  
Db 7 HFEVFNVPSCIC 19

RESULT 14  
US-08-793-792-11

;; Sequence 11, Application US/08793792  
;; Patent No. 6077511  
;; GENERAL INFORMATION:  
;; APPLICANT:  
;; TITLE OF INVENTION: Antigenic peptides derived from the  
;; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis  
;; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.  
;; NUMBER OF SEQUENCES: 13  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/793,792  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 37 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
US-08-793-792-11

Query Match 26.5%; Score 13; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HFEVFNVPSCIC 28  
| | | | | | | | | |  
Db 8 HFEVFNVPSCIC 20

RESULT 15  
US-08-836-504A-5  
;; Sequence 5, Application US/08836504A  
;; Patent No. 6130091  
;; GENERAL INFORMATION:  
;; APPLICANT: Binz, Hans  
;; APPLICANT: Nguyen Ngoc, Thien  
;; APPLICANT: Stahl, Stefan  
;; APPLICANT: Uhlen, Mathias  
;; APPLICANT: Nygren, Per Ake  
;; TITLE OF INVENTION: Method for obtaining a peptide derived  
;; TITLE OF INVENTION: from the respiratory syncytial virus, polypeptide and  
;; TITLE OF INVENTION: bacteria expressing it, and their applications as  
;; NUMBER OF SEQUENCES: 11  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Rockey, Milnamow & Katz  
;; STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,  
;; CITY: Chicago  
;; STATE: IL  
;; COUNTRY: USA  
;; ZIP: 60601  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/836,504A  
;; FILING DATE: 07-MAY-1997  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Katz, Martin L.  
;; REGISTRATION NUMBER: 25,011  
;; REFERENCE/DOCKET NUMBER: PIE1514P02000S

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-836-504A-5

Query Match 24.5%; Score 12; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.7e-06;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 SICSNPTCWA 37  
Db 15 SICSNPTCWA 26

Search completed: May 21, 2001, 14:17:54  
Job time: 82 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:16:42 ; Search time 13.03 Seconds  
(without alignments)  
258.436 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 49

Sequence: 1 KORONKPPSKPNDFEYF.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: OLIGO

Gapop 60.0 , Gapext 50.0

Searched: 198801 seqs, 68722935 residues

Word size : 0

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR\_67.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	298	1	MGNZ
2	48	98.0	297	2	major surface glyc
3	48	98.0	297	2	attachment protein
4	40	81.6	297	2	attachment protein
5	40	81.6	297	2	attachment protein
6	40	81.6	298	1	major surface glyc
7	40	81.6	298	2	G protein - Human
8	35	71.4	297	2	attachment protein
9	33	67.3	298	2	attachment protein
10	13	26.5	292	1	major surface glyc
11	13	26.5	292	1	major surface glyc
12	7	14.3	1255	1	structural polypro
13	7	14.3	1468	2	hypothetical prote
14	6	12.2	23	2	stylar glycoprotei
15	6	12.2	92	2	fibrinogen gamma c
16	6	12.2	94	2	hypothetical prote
17	6	12.2	126	2	ribosomal protein
18	6	12.2	159	2	2K688.1 protein -
19	6	12.2	191	2	hypothetical prote
20	6	12.2	196	2	stylar glycoprotei
21	6	12.2	196	2	self-incompatibili
22	6	12.2	205	2	hypothetical prote
23	6	12.2	206	2	probable NADH-plas
24	6	12.2	212	2	probable DNA prima
25	6	12.2	218	2	DNA primase (dnaE)
26	6	12.2	219	2	adhesive protein -
27	6	12.2	229	2	hypothetical prote
28	6	12.2	244	2	coat protein - gar
29	6	12.2	278	2	ribosomal protein

30	6	12.2	301	2	S62459	hypothetical prote
31	6	12.2	317	2	T32857	hypothetical prote
32	6	12.2	342	2	T25637	hypothetical prote
33	6	12.2	363	2	S67247	hypothetical prote
34	6	12.2	370	2	H64545	lipopolysaccharide
35	6	12.2	444	2	S05313	fibrinogen gamma-B
36	6	12.2	451	2	S33612	isocitrate dehydro
37	6	12.2	508	2	A29605	protein A precurs
38	6	12.2	524	1	QVSAA	probable phenylala
39	6	12.2	544	2	S75388	hypothetical prote
40	6	12.2	614	2	T19963	cytochrome-c oxida
41	6	12.2	616	2	JK0140	potassium channel
42	6	12.2	625	2	S13919	DNA repair protein
43	6	12.2	631	2	A54659	type III DNA modif
44	6	12.2	641	2	F71810	hypothetical prote
45	6	12.2	740	2	T22638	hypothetical prote
46	6	12.2	1199	2	T33337	hypothetical prote
47	6	12.2	1232	2	T05322	hypothetical prote
48	6	12.2	1249	2	A56511	myosin I myoA - Em
49	6	12.2	1254	1	VHWVVE	structural polypro
50	6	12.2	1254	1	VHWVVT	structural polypro
51	6	12.2	1254	1	QJ1978	structural polypro
52	6	12.2	1254	1	QJ1979	structural polypro
53	6	12.2	1255	1	B44213	structural polypro
54	6	12.2	1261	2	S75130	sensory transducti
55	6	12.2	1273	2	T38292	hypothetical prote
56	6	12.2	1277	2	T30532	neural cell adhesi
57	6	12.2	1651	2	B43081	vitellogenin vit-6
58	6	12.2	1896	1	RNFF2L	DNA-directed RNA p
59	5	10.2	21	2	FQ0145	glucan endo-1,3-be
60	5	10.2	25	2	A48363	2-hydroxyglutaryl-
61	5	10.2	49	2	B81933	hypothetical prote
62	5	10.2	53	2	S56728	calcium-dependent
63	5	10.2	61	2	C70245	hypothetical prote
64	5	10.2	65	2	S77542	hypothetical prote
65	5	10.2	74	2	S00302	sok protein - Esch
66	5	10.2	75	1	QOBE36	BLF1 protein - hu
67	5	10.2	84	2	C81037	hypothetical prote
68	5	10.2	96	2	A37236	I-309 protein prec
69	5	10.2	101	2	A71902	hypothetical prote
70	5	10.2	101	2	T60918	brain factor-3 - r
71	5	10.2	103	2	C72718	hypothetical prote
72	5	10.2	105	2	T26718	hypothetical prote
73	5	10.2	106	2	S51626	FRAC-3 protein -
74	5	10.2	108	2	S31977	Ig kappa chain - h
75	5	10.2	108	2	B48924	forkhead transcrip
76	5	10.2	109	2	S31998	Ig kappa chain - h
77	5	10.2	111	2	E56556	fork head homolog
78	5	10.2	112	2	D49846	spal3 protein - Sh
79	5	10.2	117	2	I49674	forkhead transcrip
80	5	10.2	121	2	B39926	hypothetical prote
81	5	10.2	121	2	B48343	hypothetical 13K p
82	5	10.2	123	2	S18470	wnt protein homolo
83	5	10.2	123	2	S54857	small nuclear ribo
84	5	10.2	124	2	C48234	hypothetical prote
85	5	10.2	124	2	C75433	hypothetical prote
86	5	10.2	126	1	B42294	holo-lacyl-carrier
87	5	10.2	132	2	T27247	hypothetical prote
88	5	10.2	136	2	JU0044	hypothetical 15.8K
89	5	10.2	139	2	T46457	NADH dehydrogenase
90	5	10.2	141	2	T11270	hypothetical prote
91	5	10.2	142	2	T28834	30S ribosomal prot
92	5	10.2	143	2	T46122	hypothetical prote
93	5	10.2	144	2	B64516	hypothetical prote
94	5	10.2	146	2	B84083	nitrogen fixation
95	5	10.2	147	1	E70019	iron-sulfur cofact
96	5	10.2	151	2	S71430	DNA repair protein
97	5	10.2	152	2	S27791	hypothetical prote
98	5	10.2	155	2	T33305	homeotic protein H
99	5	10.2	155	2	S25846	probable membrane
100	5	10.2	158	2	S53572	hypothetical prote
101	5	10.2	158	2	T27577	ribosomal protein
102	5	10.2	159	2	S16577	

103	5	10.2	159	2	T23149	hypothetical prote	176	5	10.2	239	2	T20515	hypothetical prote
104	5	10.2	162	2	D38257	glucan endo-1,3-be	177	5	10.2	240	2	S77884	hypothetical prote
105	5	10.2	162	2	E38257	glucan endo-1,3-be	178	5	10.2	241	2	D43273	hergulin precurs
106	5	10.2	166	2	E71040	hypothetical prote	179	5	10.2	242	2	H1883	hydrogenase expres
107	5	10.2	167	2	I50487	ubiquinol--cytochr	180	5	10.2	242	2	D64632	hydrogenase expres
108	5	10.2	167	2	F70478	hypothetical prote	181	5	10.2	243	2	JC4585	GTP cyclohydrolase
109	5	10.2	169	2	T47558	hypothetical prote	182	5	10.2	243	2	T34680	hypothetical prote
110	5	10.2	171	2	D75174	hypothetical prote	183	5	10.2	244	2	T49893	glycine-rich prote
111	5	10.2	173	2	S47171	gene PR-1 protein	184	5	10.2	246	2	S35620	ribosomal protein
112	5	10.2	175	2	I38408	neu differentiatio	185	5	10.2	247	1	KHUCM	chymase (EC 3.4.21
113	5	10.2	175	2	D83304	conserved hypothet	186	5	10.2	248	2	S49323	chymotrypsin (EC 3
114	5	10.2	177	2	T12717	hypothetical prote	187	5	10.2	248	2	T41608	hypothetical prote
115	5	10.2	178	2	T09585	high mobility grou	188	5	10.2	249	1	A35842	chymase (EC 3.4.21
116	5	10.2	178	2	T09584	high mobility grou	189	5	10.2	250	2	S74495	hypothetical prote
117	5	10.2	178	2	E81151	conserved hypothet	190	5	10.2	251	2	S27910	coat protein - gar
118	5	10.2	179	2	I40754	GTP cyclohydrolase	191	5	10.2	251	2	JQ2173	viral coat 27.6K p
119	5	10.2	181	2	T48558	hypothetical prote	192	5	10.2	253	2	S33820	secretory protein
120	5	10.2	182	2	E69401	phenylacrylic acid	193	5	10.2	253	2	C36808	hypothetical prote
121	5	10.2	190	2	A81438	GTP cyclohydrolase	194	5	10.2	254	2	A64437	hypothetical prote
122	5	10.2	191	2	E36889	probable 3-isoprop	195	5	10.2	259	2	T45841	6-phosphogluconol
123	5	10.2	191	2	A81870	hypothetical prote	196	5	10.2	259	2	C82153	probable PTS syste
124	5	10.2	191	2	T17995	hypothetical prote	197	5	10.2	260	2	A71949	nh(3)-dependent na
125	5	10.2	194	2	T15927	hypothetical prote	198	5	10.2	260	2	A64561	NH(3)-dependent NA
126	5	10.2	196	2	S50487	hypothetical prote	199	5	10.2	262	2	T22371	hypothetical prote
127	5	10.2	199	2	T29943	hypothetical prote	200	5	10.2	265	2	T42419	hypothetical prote
128	5	10.2	200	2	T07149	systemin precursor	201	5	10.2	265	2	T40259	hypothetical prote
129	5	10.2	201	2	B72380	hypothetical prote	202	5	10.2	269	2	T18145	hypothetical prote
130	5	10.2	201	2	A64737	yadL protein - Esc	203	5	10.2	269	2	S74024	hypothetical prote
131	5	10.2	202	2	T49309	hypothetical prote	204	5	10.2	273	1	EDBE12	immediate-early pr
132	5	10.2	202	2	T34287	hypothetical prote	205	5	10.2	273	2	F71645	hypothetical prote
133	5	10.2	203	2	A49647	GTP-binding protei	206	5	10.2	273	2	T40611	hypothetical prote
134	5	10.2	203	2	T48129	hypothetical prote	207	5	10.2	273	2	T33424	hypothetical prote
135	5	10.2	205	2	I46876	phosphoprotein pho	208	5	10.2	274	2	E81319	probable glucosylt
136	5	10.2	206	2	T06852	hypothetical prote	209	5	10.2	274	2	S69561	hypothetical prote
137	5	10.2	209	1	S48459	probable dual spec	210	5	10.2	275	2	A69413	conserved hypothet
138	5	10.2	211	2	D50111	hypothetical prote	211	5	10.2	276	2	T38825	hypothetical prote
139	5	10.2	213	2	S29924	cyclin 1 - alfalfa	212	5	10.2	278	2	S16678	Lyl-1 protein - mo
140	5	10.2	214	2	S74854	hypothetical prote	213	5	10.2	279	2	B72255	dimethyladenosine
141	5	10.2	214	2	B70470	hypothetical prote	214	5	10.2	279	2	C70458	diaminopimelate ep
142	5	10.2	215	2	T22446	hypothetical prote	215	5	10.2	279	2	T16736	hypothetical prote
143	5	10.2	216	2	H82608	transcription regu	216	5	10.2	281	1	B47629	cell surface glyco
144	5	10.2	218	1	HSC11	histone H1.02 - ch	217	5	10.2	282	2	G64479	hypothetical prote
145	5	10.2	218	2	A23055	histone H1.01 - ch	218	5	10.2	284	2	T42608	immediate-early pr
146	5	10.2	218	2	S01262	histone H1 - musco	219	5	10.2	285	2	A34469	envelope protein p
147	5	10.2	219	2	C65074	hypothetical prote	220	5	10.2	285	2	B82459	hypothetical prote
148	5	10.2	220	2	I50588	fibroblast growth	221	5	10.2	286	2	S07193	chorion protein s3
149	5	10.2	220	2	E71857	probable outer mem	222	5	10.2	286	2	T24233	hypothetical prote
150	5	10.2	223	2	T21669	hypothetical prote	223	5	10.2	288	2	B45580	transcription fact
151	5	10.2	223	2	H65165	hypothetical 22.0	224	5	10.2	288	2	S26028	NADH dehydrogenase
152	5	10.2	223	2	D69311	conserved hypothet	225	5	10.2	290	2	S26028	5,10-methylenetr
153	5	10.2	224	2	JN0798	restriction endonu	226	5	10.2	292	1	H64123	hypothetical prote
154	5	10.2	225	1	A25910	small nuclear ribo	227	5	10.2	292	2	S52888	SUB1 protein - yea
155	5	10.2	225	2	S66212	triose-phosphate i	228	5	10.2	293	2	S09209	chorion protein s3
156	5	10.2	226	2	F82052	phosphoglycolate p	229	5	10.2	294	2	J70536	ADP-ribosyl-nitro
157	5	10.2	226	2	T23233	hypothetical prote	230	5	10.2	295	2	T34572	hypothetical prote
158	5	10.2	228	2	C75025	triose-phosphate i	231	5	10.2	296	2	T21070	hypothetical prote
159	5	10.2	228	2	S19932	glycine-rich prote	232	5	10.2	297	2	T18638	hypothetical prote
160	5	10.2	229	1	C45345	vif protein - capr	233	5	10.2	298	2	T33046	hypothetical prote
161	5	10.2	229	1	B43685	nonstructural prot	234	5	10.2	299	2	B55527	pqqG protein - Met
162	5	10.2	229	2	B40621	nisin biosynthesis	235	5	10.2	300	2	A43521	lymphocyte surface
163	5	10.2	229	2	B70158	conserved hypothet	236	5	10.2	300	2	G69476	hypothetical prote
164	5	10.2	230	2	A56210	neu differentiatio	237	5	10.2	302	1	P3WMCC	3a protein - cowpe
165	5	10.2	231	2	G71201	triose-phosphate i	238	5	10.2	302	2	T36903	probable dihydriol
166	5	10.2	232	2	T09003	response regulator	239	5	10.2	302	2	S69725	hypothetical prote
167	5	10.2	232	2	D71442	hypothetical prote	240	5	10.2	302	2	T24187	hypothetical prote
168	5	10.2	233	2	C82360	cell division ATP-	241	5	10.2	304	2	G81417	cytochrome-c perox
169	5	10.2	233	2	S50154	hypothetical prote	242	5	10.2	304	2	T42521	probable UTP--gluc
170	5	10.2	235	1	A59036	cytochrome c554, t	243	5	10.2	304	2	T29184	hypothetical prote
171	5	10.2	236	1	A35649	cell surface prote	244	5	10.2	305	2	A69669	oligopeptide ABC t
172	5	10.2	236	1	A46472	cell surface prote	245	5	10.2	305	2	H82888	methionyl-tRNA for
173	5	10.2	238	1	A34378	endothelin 3 precu	246	5	10.2	307	2	T00687	hypothetical prote
174	5	10.2	238	1	S74682	spore germination	247	5	10.2	309	2	D71173	probable modifical
175	5	10.2	238	2	S33314	hypothetical prote	248	5	10.2	309	2	S57102	hypothetical prote

249	5	10.2	309	2	A70194	ABC transporter, A	322	5	10.2	370	2	S54297	protein phosphatas
250	5	10.2	309	2	T45719	hypothetical prote	323	5	10.2	370	2	G64654	hypothetical prote
251	5	10.2	310	2	JL0091	beta-lactamase (EC	324	5	10.2	371	1	AJMSQ3	glutamate--ammonia
252	5	10.2	310	2	S40808	polynucleotide ade	325	5	10.2	372	2	A42778	agglutinin precurs
253	5	10.2	310	2	B64882	conserved hypothet	326	5	10.2	373	1	AJMSO	glutamate--ammonia
254	5	10.2	310	2	A69457	hypothetical prote	327	5	10.2	373	2	A70334	hypothetical prote
255	5	10.2	312	2	T47497	hypothetical prote	328	5	10.2	374	2	D72288	hypothetical prote
256	5	10.2	314	2	A71858	pyruvate ferredoxi	329	5	10.2	376	2	E31751	protein kinase cat
257	5	10.2	315	2	C83945	stage V sporulatio	330	5	10.2	378	2	S71201	biotin synthase (E
258	5	10.2	316	1	PBNSLC	beta-lactamase (EC	331	5	10.2	379	1	CBBO	ubiquinol--cytochr
259	5	10.2	318	2	T48507	probable GTP-bindi	332	5	10.2	379	1	S17419	ubiquinol--cytochr
260	5	10.2	318	2	H71406	probable reverse t	333	5	10.2	379	1	S17405	ubiquinol--cytochr
261	5	10.2	319	2	S62810	adenine specific d	334	5	10.2	379	1	S43267	ubiquinol--cytochr
262	5	10.2	319	2	T21804	hypothetical prote	335	5	10.2	379	1	S43265	ubiquinol--cytochr
263	5	10.2	320	2	S09208	chorion protein s3	336	5	10.2	379	1	S17409	ubiquinol--cytochr
264	5	10.2	320	2	T25271	hypothetical prote	337	5	10.2	379	1	S43266	ubiquinol--cytochr
265	5	10.2	320	2	T37990	probable polysacch	338	5	10.2	379	1	S43268	ubiquinol--cytochr
266	5	10.2	322	2	T27966	hypothetical prote	339	5	10.2	379	1	S17414	ubiquinol--cytochr
267	5	10.2	322	2	T16633	hypothetical prote	340	5	10.2	379	1	S17407	ubiquinol--cytochr
268	5	10.2	323	2	S72915	hypothetical prote	341	5	10.2	379	1	S43269	ubiquinol--cytochr
269	5	10.2	324	2	S18547	alkanal monooxygen	342	5	10.2	379	1	S17413	ubiquinol--cytochr
270	5	10.2	324	2	A23866	transcription repr	343	5	10.2	379	1	S17418	ubiquinol--cytochr
271	5	10.2	325	2	A69595	probable modD prot	344	5	10.2	379	1	S17415	ubiquinol--cytochr
272	5	10.2	325	2	D70866	CCCH zinc finger p	345	5	10.2	379	1	S43263	ubiquinol--cytochr
273	5	10.2	325	2	S57977	hypothetical prote	346	5	10.2	379	1	S43262	ubiquinol--cytochr
274	5	10.2	325	2	T23208	Ig gamma-2 chain C	347	5	10.2	379	1	S17417	ubiquinol--cytochr
275	5	10.2	327	2	S06611	glucan endo-1,3-be	348	5	10.2	379	1	S43261	ubiquinol--cytochr
276	5	10.2	331	2	T02343	hypothetical prote	349	5	10.2	379	1	S41832	ubiquinol--cytochr
277	5	10.2	331	2	T18614	probable anion-upt	350	5	10.2	379	1	S43264	ubiquinol--cytochr
278	5	10.2	331	2	H81300	hypothetical prote	351	5	10.2	379	1	S43270	ubiquinol--cytochr
279	5	10.2	331	2	C64515	hypothetical prote	352	5	10.2	379	1	S17420	ubiquinol--cytochr
280	5	10.2	331	2	T13992	Sf16 protein, poll	353	5	10.2	379	1	S17406	ubiquinol--cytochr
281	5	10.2	332	2	A69224	polyferredoxin 4x2	354	5	10.2	379	2	E58851	ubiquinol--cytochr
282	5	10.2	332	2	H81876	probable membrane	355	5	10.2	379	2	S58057	ubiquinol--cytochr
283	5	10.2	332	2	B70965	probable integrase	356	5	10.2	379	2	S58085	ubiquinol--cytochr
284	5	10.2	333	2	S15238	O-antigen acetylase	357	5	10.2	379	2	S58448	ubiquinol--cytochr
285	5	10.2	334	2	B81406	probable integral	358	5	10.2	379	2	T11492	ubiquinol--cytochr
286	5	10.2	336	2	D69074	polyferredoxin 4x2	359	5	10.2	379	2	T10998	ubiquinol--cytochr
287	5	10.2	336	2	D70113	basic membrane pro	360	5	10.2	379	2	T11453	ubiquinol--cytochr
288	5	10.2	338	2	C64099	arDpGlucose 4,6-de	361	5	10.2	379	2	T11152	ubiquinol--cytochr
289	5	10.2	340	2	T28110	hypothetical prote	362	5	10.2	380	1	CBRT	ubiquinol--cytochr
290	5	10.2	341	2	S74759	hypothetical prote	363	5	10.2	380	1	S04840	ubiquinol--cytochr
291	5	10.2	342	2	T49687	lipoyltransferase	364	5	10.2	380	1	VCVGCN	coat protein - cuc
292	5	10.2	343	2	B38257	glucan endo-1,3-be	365	5	10.2	380	2	E58893	ubiquinol--cytochr
293	5	10.2	343	2	S50680	beta-1,3 glucanase	366	5	10.2	380	2	S70594	ubiquinol--cytochr
294	5	10.2	346	2	S55403	cymA protein precu	367	5	10.2	380	2	T11113	ubiquinol--cytochr
295	5	10.2	347	1	F64937	probable L-iditol	368	5	10.2	380	2	T11114	ubiquinol--cytochr
296	5	10.2	347	2	T07140	glucan endo-1,3-be	369	5	10.2	380	2	T11299	ubiquinol--cytochr
297	5	10.2	347	2	E83525	TolA protein PA097	370	5	10.2	380	2	S22415	membrane protein T
298	5	10.2	349	2	H82643	alcohol dehydrogen	371	5	10.2	380	2	T34568	hypothetical prote
299	5	10.2	349	2	S57453	polyferredoxin 4x2	372	5	10.2	380	2	T51053	hypothetical prote
300	5	10.2	350	2	JL0114	nitrogen regulatio	373	5	10.2	381	1	CBMS	ubiquinol--cytochr
301	5	10.2	350	2	T22450	hypothetical prote	374	5	10.2	381	2	S68140	ubiquinol--cytochr
302	5	10.2	351	2	T20270	hypothetical prote	375	5	10.2	381	2	D71943	hypothetical prote
303	5	10.2	352	2	F82284	S-adenosylmethioni	376	5	10.2	382	1	S33573	ubiquinol--cytochr
304	5	10.2	353	2	T34312	hypothetical prote	377	5	10.2	382	2	T11138	ubiquinol--cytochr
305	5	10.2	354	2	T04262	mitogen-activated	378	5	10.2	383	2	C75153	probable n2,n2-dim
306	5	10.2	355	2	T36273	hypothetical prote	379	5	10.2	383	1	CBBY	ubiquinol--cytochr
307	5	10.2	356	2	T03249	glucan endo-1,3-be	380	5	10.2	385	1	S15157	ubiquinol--cytochr
308	5	10.2	358	2	B81452	phosphoserine tran	381	5	10.2	385	2	S78660	ubiquinol--cytochr
309	5	10.2	358	2	A70746	hypothetical prote	382	5	10.2	386	2	T11832	ubiquinol--cytochr
310	5	10.2	359	2	D70155	fructose-bisphosph	383	5	10.2	389	2	T27085	hypothetical prote
311	5	10.2	359	2	G02221	CAGRI protein - hu	384	5	10.2	389	2	T23167	hypothetical prote
312	5	10.2	359	2	T22774	hypothetical prote	385	5	10.2	389	2	T47178	hypothetical prote
313	5	10.2	359	2	T19009	hypothetical prote	386	5	10.2	390	2	T51713	probable formamido
314	5	10.2	361	1	IBHUN	hydroxymethylbilan	387	5	10.2	392	2	T34095	zinc finger protel
315	5	10.2	361	1	IBRTE	hydroxymethylbilan	388	5	10.2	393	1	S22520	myb-related protel
316	5	10.2	361	1	IBMSGN	hydroxymethylbilan	389	5	10.2	394	2	T10200	hypothetical prote
317	5	10.2	362	2	B64527	M-protein - Helico	390	5	10.2	398	2	C82614	riboflavin biosynt
318	5	10.2	363	2	T26700	hypothetical prote	391	5	10.2	398	2	T46312	hypothetical prote
319	5	10.2	363	2	H71568	hypothetical prote	392	5	10.2	399	1	B49836	transcription fact
320	5	10.2	365	2	F64577	type I restriction	393	5	10.2	399	1	A43685	polymerase-associa
321	5	10.2	365	2	S72924	hypothetical prote	394	5	10.2	402	2	A40678	T-cell adhesio re

395	5	10.2	402	2	S46641	probable membrane	468	5	10.2	488	2	A83367	probable phosphoma
396	5	10.2	405	2	S46828	probable GTP-bind	469	5	10.2	488	2	E70234	conserved hypotet
397	5	10.2	407	2	E71665	bicyclomycin resis	470	5	10.2	491	2	A41632	histamine H1 recep
398	5	10.2	408	2	T47498	hypothetical prote	471	5	10.2	494	2	JE0353	uridine diphosphog
399	5	10.2	409	2	G71935	type I restriction	472	5	10.2	498	2	A48203	interleukin-14 pre
400	5	10.2	410	2	T52294	patatin-like prote	473	5	10.2	498	2	H83505	deoxyguanosinetrip
401	5	10.2	411	2	S58094	hypothetical WW do	474	5	10.2	503	2	T24985	hypothetical prote
402	5	10.2	415	2	B69875	conserved hypotet	475	5	10.2	503	2	T13006	betaine aldehyde d
403	5	10.2	416	2	A41694	regulatory protein	476	5	10.2	503	2	A54868	nuclear respirator
404	5	10.2	416	2	T24564	hypothetical prote	477	5	10.2	504	2	F64143	probable GPase/GT
405	5	10.2	419	2	B71481	probable clp prote	478	5	10.2	506	2	T40935	probable utp-gluc
406	5	10.2	419	2	B64633	hypothetical prote	479	5	10.2	506	2	A82876	oligopeptide trans
407	5	10.2	419	2	C71900	hypothetical prote	480	5	10.2	507	2	S73199	proteochlorophyllid
408	5	10.2	420	1	S34379	glycine hydroxymet	481	5	10.2	508	2	E64089	probable transport
409	5	10.2	420	1	S22418	calsequestrin prec	482	5	10.2	508	2	S59870	fork head domain p
410	5	10.2	421	1	D64100	glycine hydroxymet	483	5	10.2	508	2	A31637	transcription fact
411	5	10.2	422	2	H64489	hypothetical prote	484	5	10.2	509	1	SI4629	aldehyde dehydroge
412	5	10.2	422	2	S23237	glial growth facto	485	5	10.2	509	2	S76731	hypothetical prote
413	5	10.2	425	2	T46969	DEAD box RNA helic	486	5	10.2	512	2	G70662	probable plcb prot
414	5	10.2	425	2	T00720	hypothetical prote	487	5	10.2	513	2	T02002	hypothetical prote
415	5	10.2	426	2	T34108	hypothetical prote	488	5	10.2	518	2	T39311	probable pre-mrna
416	5	10.2	426	2	T51373	hypothetical prote	489	5	10.2	519	2	T16712	hypothetical prote
417	5	10.2	427	2	JN0785	Carbon catabolite	490	5	10.2	526	2	T51372	hypothetical prote
418	5	10.2	428	2	S56679	mitosis-specific c	491	5	10.2	527	2	T49241	pectinesterase-lik
419	5	10.2	429	2	A83463	flagellar biosynth	492	5	10.2	529	2	A56516	nuclear localizati
420	5	10.2	430	2	T25489	hypothetical prote	493	5	10.2	530	2	T52508	hypothetical prote
421	5	10.2	431	2	G70344	probable glucose-6	494	5	10.2	534	2	D83775	hypothetical prote
422	5	10.2	431	2	T37621	hypothetical prote	495	5	10.2	535	2	T13645	hypothetical prote
423	5	10.2	433	2	S51773	transcription fact	496	5	10.2	537	2	A35400	surface protein T6
424	5	10.2	436	2	B48937	cysteine aminopept	497	5	10.2	540	2	S44830	F54F2.5 protein -
425	5	10.2	437	2	B46361	p element homolog	498	5	10.2	542	2	S58837	hypothetical prote
426	5	10.2	437	2	J50237	hypothetical 48K p	499	5	10.2	542	2	T48488	hypothetical prote
427	5	10.2	438	1	HVRK62	Ig mu chain C regi	500	5	10.2	544	2	T43364	potassium channel
428	5	10.2	443	2	T30619	probable serine/th	501	5	10.2	549	2	F64972	hypothetical prote
429	5	10.2	448	2	S15018	transcription fact	502	5	10.2	550	2	G70768	hypothetical prote
430	5	10.2	448	2	A72089	integral membrane	503	5	10.2	552	2	T25593	hypothetical prote
431	5	10.2	450	2	T15154	hypothetical prote	504	5	10.2	556	2	D69676	phosphodiesterase/
432	5	10.2	451	1	ACBOG2	gamma-aminobutyric	505	5	10.2	561	2	S64068	hypothetical prote
433	5	10.2	451	2	JH0370	gamma-aminobutyric	506	5	10.2	565	1	VHIVC8	nucleoprotein - in
434	5	10.2	451	2	I57947	gamma-aminobutyric	507	5	10.2	565	2	H71982	hypothetical prote
435	5	10.2	451	2	A81581	ABC transporter, p	508	5	10.2	566	1	T64243	hypothetical prote
436	5	10.2	452	2	T00113	undecaprenyl-phos	509	5	10.2	567	2	T01032	hypothetical prote
437	5	10.2	453	2	T30985	hypothetical prote	510	5	10.2	568	2	S74481	probable phosphoe
438	5	10.2	454	2	T20829	probable serine ca	511	5	10.2	569	2	T02435	probable oxysterol
439	5	10.2	455	2	S56695	1-aminocyclopropan	512	5	10.2	571	2	T00835	calcium-dependent
440	5	10.2	455	2	F72336	hemolysin-related	513	5	10.2	576	2	T43363	potassium channel
441	5	10.2	455	2	JC1224	nucleobindin precu	514	5	10.2	577	2	T07375	glucose-6-phosphat
442	5	10.2	456	2	S20597	ribonuclease inhib	515	5	10.2	582	2	T40198	transposase - Bact
443	5	10.2	457	2	S55091	probable membrane	516	5	10.2	585	2	T37526	probable transcrip
444	5	10.2	458	2	T10096	nifN protein - Met	517	5	10.2	586	1	AJPMN1	asparagine synthas
445	5	10.2	460	2	T33420	hypothetical prote	518	5	10.2	586	2	S69182	asparagine synthas
446	5	10.2	461	2	S34472	MFH-1 protein - mo	519	5	10.2	586	2	S66697	probable membrane
447	5	10.2	461	2	H71717	3-deoxy-d-manno-oc	520	5	10.2	588	2	T33815	hypothetical prote
448	5	10.2	462	2	T38404	neu differentiation	521	5	10.2	590	2	S25165	asparagine synthas
449	5	10.2	464	2	B72260	conserved hypotet	522	5	10.2	592	2	T50154	probable 6-phospho
450	5	10.2	464	2	S67069	hypothetical prote	523	5	10.2	593	2	F64523	hypothetical prote
451	5	10.2	466	1	CYDKD1	delta-1-crystallin	524	5	10.2	593	2	T24379	hypothetical prote
452	5	10.2	466	2	JN0486	argininosuccinate	525	5	10.2	601	2	T42251	polypeptide N-acet
453	5	10.2	466	2	T29353	hypothetical prote	526	5	10.2	603	1	E64054	probable 5'-nucleo
454	5	10.2	468	1	CYDKD2	delta-2-crystallin	527	5	10.2	603	2	T33134	hypothetical prote
455	5	10.2	470	2	T31465	cell cycle protein	528	5	10.2	604	2	T45627	replication factor
456	5	10.2	472	1	A49836	transcription fact	529	5	10.2	605	2	S67815	protein-tyrosine k
457	5	10.2	472	2	T27903	hypothetical prote	530	5	10.2	609	1	A48070	heat shock transcr
458	5	10.2	474	2	S31712	beta-1,3-glucanase	531	5	10.2	610	1	A49082	calcium-dependent
459	5	10.2	476	2	JC5042	G protein-coupled	532	5	10.2	612	2	E81287	probable sugar tra
460	5	10.2	478	2	T11318	NADH dehydrogenase	533	5	10.2	612	2	T29761	hypothetical prote
461	5	10.2	481	1	S57294	carboxypeptidase D	534	5	10.2	622	2	T59172	SPC72 protein - ye
462	5	10.2	482	2	G71603	chromatin-binding	535	5	10.2	623	2	T39001	probable exonuclea
463	5	10.2	482	2	S56945	protein YJH162c -	536	5	10.2	628	2	S44629	F22B7, 10 protein -
464	5	10.2	484	2	D64214	hypothetical prote	537	5	10.2	630	2	A70117	probable long-chai
465	5	10.2	485	2	S64945	probable membrane	538	5	10.2	630	2	T07966	probable ethylene
466	5	10.2	486	2	T20482	hypothetical prote	539	5	10.2	633	2	J01242	Viral replicase 2
467	5	10.2	487	2	JC2495	histamine H1 recep	540	5	10.2	635	2	F70874	probable membrane



687	5	10.2	961	2	T23095	hypothetical prote	760	5	10.2	1328	1	S04273	retrovirus-related
688	5	10.2	970	2	S63059	hypothetical prote	761	5	10.2	1330	2	A36373	hypothetical prote
689	5	10.2	973	2	T41201	isooleucyl-tRNA syn	762	5	10.2	1353	2	T00347	hypothetical prote
690	5	10.2	975	2	T48107	hypothetical prote	763	5	10.2	1358	2	S33653	probable serine/th
691	5	10.2	976	2	S45738	pleiotropic drug r	764	5	10.2	1367	2	S51959	hypothetical prote
692	5	10.2	992	2	S54396	protein L precursor	765	5	10.2	1367	2	T18466	hypothetical prote
693	5	10.2	996	2	S70646	transcription fact	766	5	10.2	1380	2	S57150	ZMS1 protein - yea
694	5	10.2	1001	2	S74544	translation initia	767	5	10.2	1385	2	T25828	hypothetical prote
695	5	10.2	1002	2	S62035	isooleucine--tRNA l	768	5	10.2	1390	2	T30346	insulin receptor -
696	5	10.2	1003	2	C71139	hypothetical prote	769	5	10.2	1405	2	T40607	probable dna-direc
697	5	10.2	1007	2	T24643	hypothetical prote	770	5	10.2	1419	1	DVZQF	multidrug resistanc
698	5	10.2	1008	2	T04462	hypothetical prote	771	5	10.2	1428	2	T13926	probable protein p
699	5	10.2	1021	2	G75403	DNA topoisomerase	772	5	10.2	1429	2	T19422	hypothetical prote
700	5	10.2	1036	2	T38734	hypothetical prote	773	5	10.2	1440	2	JC6312	protein-tyrosine-p
701	5	10.2	1037	2	T13350	transcription fact	774	5	10.2	1468	2	S58250	DNA-directed DNA p
702	5	10.2	1039	2	T28905	hypothetical prote	775	5	10.2	1471	1	S30790	myosin MFO4 - yea
703	5	10.2	1051	2	T43233	carbamoyl-phosphat	776	5	10.2	1477	2	T18534	protein-tyrosine k
704	5	10.2	1052	2	C84221	hypothetical 114K	777	5	10.2	1479	2	T17401	transcription regu
705	5	10.2	1059	2	G83706	antibiotic mercap	778	5	10.2	1482	2	T34010	hypothetical prote
706	5	10.2	1062	2	S09834	hypothetical prote	779	5	10.2	1492	2	T18560	DNA-directed DNA p
707	5	10.2	1076	1	A35622	nuclear pore prote	780	5	10.2	1513	2	T31434	densin-180 - rat
708	5	10.2	1083	2	T23031	hypothetical prote	781	5	10.2	1513	2	T28158	probable DNA-direc
709	5	10.2	1084	2	S23319	hypothetical prote	782	5	10.2	1525	1	GNWVS	genome polypeptin
710	5	10.2	1086	2	S54876	NAD(P)+ transhydro	783	5	10.2	1539	2	T48059	ABC transporter-li
711	5	10.2	1086	2	S74251	phosphorylase kina	784	5	10.2	1570	2	T18272	1-phosphatidylinos
712	5	10.2	1093	2	S74250	phosphorylase kina	785	5	10.2	1603	1	VJKW5	vitellogenin vit-5
713	5	10.2	1098	1	YGBSGL	phenylalanine race	786	5	10.2	1650	2	T27864	hypothetical prote
714	5	10.2	1104	1	A36866	microbial collagen	787	5	10.2	1672	2	T46237	hypothetical prote
715	5	10.2	1106	2	T18759	hypothetical prote	788	5	10.2	1683	2	T30885	complement compone
716	5	10.2	1106	2	T31742	hypothetical prote	789	5	10.2	1700	2	S08167	Balbani ring 3 pr
717	5	10.2	1107	2	T20578	hypothetical prote	790	5	10.2	1712	2	C71618	hypothetical prote
718	5	10.2	1113	2	H84105	hypothetical prote	791	5	10.2	1717	2	T50247	probable helicase
719	5	10.2	1119	2	T20577	hypothetical prote	792	5	10.2	1752	2	T48965	hypothetical prote
720	5	10.2	1122	2	T47424	hypothetical prote	793	5	10.2	1772	2	A45532	major merozoite su
721	5	10.2	1127	2	T25804	hypothetical prote	794	5	10.2	1872	2	T00339	hypothetical prote
722	5	10.2	1131	2	T19442	hypothetical prote	795	5	10.2	1873	2	A30063	dihydropyridine re
723	5	10.2	1134	2	T20332	hypothetical prote	796	5	10.2	1906	1	S68235	myosin-light-chain
724	5	10.2	1140	2	T20984	hypothetical prote	797	5	10.2	1974	2	T30010	hypothetical prote
725	5	10.2	1144	1	A43271	nitric-oxide synth	798	5	10.2	2077	2	T43991	large tegument pro
726	5	10.2	1144	2	A36968	PI-like adhesin pr	799	5	10.2	2077	2	T44178	large tegument pro
727	5	10.2	1147	1	S47647	nitric-oxide synth	800	5	10.2	2136	2	A05037	hypothetical prote
728	5	10.2	1147	1	I56575	nitric-oxide synth	801	5	10.2	2144	2	S71490	ash1 protein - fru
729	5	10.2	1147	1	S38253	nitric-oxide synth	802	5	10.2	2206	1	GNNY21	genome polypeptin
730	5	10.2	1147	1	I53165	nitric-oxide synth	803	5	10.2	2207	1	GNNY1P	genome polypeptin
731	5	10.2	1147	2	JC5027	nitric-oxide synth	804	5	10.2	2209	1	GNNY2P	genome polypeptin
732	5	10.2	1147	2	JC5028	nitric-oxide synth	805	5	10.2	2209	1	GNNY3P	genome polypeptin
733	5	10.2	1147	2	JC5029	nitric-oxide synth	806	5	10.2	2214	1	A48548	genome polypeptin
734	5	10.2	1147	2	S65440	nitric-oxide synth	807	5	10.2	2298	2	T49648	hypothetical prote
735	5	10.2	1151	2	T18535	high molecular mas	808	5	10.2	2301	1	GNNYTN	genome polypeptin
736	5	10.2	1154	2	S43275	hypothetical prote	809	5	10.2	2303	1	GNNYTM	genome polypeptin
737	5	10.2	1169	2	C71639	hypothetical prote	810	5	10.2	2303	1	GNNYTP	genome polypeptin
738	5	10.2	1187	1	JC4155	protein-tyrosine-p	811	5	10.2	2303	2	SI3554	genome polypeptin
739	5	10.2	1189	1	JC2386	protein-tyrosine-p	812	5	10.2	2342	2	T18200	fatty-acid synthas
740	5	10.2	1196	1	DNBEV1	major DNA-binding	813	5	10.2	2437	2	S53611	MIBP1 protein - ra
741	5	10.2	1196	1	DNBEKS	DNA-binding protei	814	5	10.2	2500	1	WMHUE2	HIV-EP2 enhancer-b
742	5	10.2	1196	1	DNBEHF	DNA-binding protei	815	5	10.2	2555	2	C69681	peptide synthetase
743	5	10.2	1197	1	A48350	DNA-binding protei	816	5	10.2	2610	2	T20968	hypothetical prote
744	5	10.2	1199	2	T18348	probable pol polyp	817	5	10.2	2630	2	T08868	polyprotein pI - A
745	5	10.2	1214	2	JC7259	Snad interacting p	818	5	10.2	2647	2	T28161	hypothetical prote
746	5	10.2	1219	2	S54570	probable membrane	819	5	10.2	2657	2	T18497	hypothetical prote
747	5	10.2	1221	2	T30529	ubiquitin carboxyl	820	5	10.2	2962	2	T19756	hypothetical prote
748	5	10.2	1230	2	T18256	probable serine/th	821	5	10.2	3122	2	T17202	DNA-directed DNA p
749	5	10.2	1230	2	T18259	serine/threonine p	822	5	10.2	3176	1	CGHU3A	collagen alpha 3(V
750	5	10.2	1240	2	T04833	hypothetical prote	823	5	10.2	3655	2	T38084	TRAP-like protein
751	5	10.2	1253	1	VHWV	structural polypo	824	5	10.2	3759	2	A35085	thiorax protein
752	5	10.2	1272	2	S60999	ubiquitin-specific	825	5	10.2	3871	2	T22812	hypothetical prote
753	5	10.2	1279	2	E64709	type IIS restricti	826	5	10.2	4377	2	A55575	ankyrin 3, long sp
754	5	10.2	1281	2	JC5368	dynactin 1 - mouse	827	5	10.2	4660	2	T42737	gp330 protein prec
755	5	10.2	1291	1	S05465	retrovirus-related	828	5	10.2	4910	2	S64942	probable membrane
756	5	10.2	1306	2	T28313	ORF MSV152 probabl	829	5	10.2	6658	2	T13931	projectin - fruit
757	5	10.2	1306	2	A60165	sodium channel pro	830	5	10.2	6805	2	S20901	titin - rabbit (fr
758	5	10.2	1321	2	S52863	DNA-binding protei	831	5	10.2	6839	2	SW7242	twitchin [similar
759	5	10.2	1325	2	S16129	dynein-associated	832	5	10.2	7160	2	T27935	hypothetical prote



979 4 8.2 58 2 S58628 hypothetical prote  
980 4 8.2 58 2 C83918 hypothetical prote  
981 4 8.2 58 2 H82736 hypothetical prote  
982 4 8.2 59 2 T12647 NADH dehydrogenase  
983 4 8.2 59 2 I51260 calactonin I - pin  
984 4 8.2 59 2 T07432 photosystem II pro  
985 4 8.2 59 2 J00811 hypothetical 6.8K  
986 4 8.2 59 2 H82107 hypothetical prote  
987 4 8.2 59 2 H69218 hypothetical prote  
988 4 8.2 60 2 D69133 DNA-dependent RNA  
989 4 8.2 60 2 F75618 hypothetical prote  
990 4 8.2 61 1 T1E8H hypothetical prote  
991 4 8.2 61 2 A71868 proteinase inhibit  
992 4 8.2 61 2 F81844 hypothetical prote  
993 4 8.2 61 2 A69524 hypothetical prote  
994 4 8.2 61 2 J01086 nodulin-14 precurs  
995 4 8.2 61 2 A45099 calcium channel al  
996 4 8.2 62 2 S42265 Ig kappa chain V r  
997 4 8.2 62 2 JN0733 hypothetical 7.5K  
998 4 8.2 62 2 D71571 hypothetical prote  
999 4 8.2 62 2 T19376 hypothetical prote  
1000 4 8.2 62 2 D83979 hypothetical prote

## ALIGNMENTS

RESULT 1  
MGZ  
major surface glycoprotein G - human respiratory syncytial virus  
C:Species: human respiratory syncytial virus  
C:Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 24-Sep-1999  
C:Accession: A94048; A93599; A04039  
R:Wertz, G.W.; Collins, P.L.; Huang, Y.; Gruber, C.; Levine, S.; Ball, L.A.  
Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985  
A:Title: Nucleotide sequence of the G protein gene of human respiratory syncytial virus  
A:Reference number: A94048; MUID:85216636  
A:Accession: A94048  
A:Molecule type: mRNA  
A:Residues: 1-298 <WER>  
A:Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217; GB:7.1; PID:g333932  
A:Note: Residues 207-298 are identical with residues 376-467 of the nucleocapsid protein  
A:Note: this protein may carry 40-80 separate O-linked carbohydrate chains distributed a  
R:Satake, M.; Coligan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S.  
Nucleic Acids Res. 13, 7795-7812, 1985  
A:Title: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure.  
A:Reference number: A93599; MUID:86067198  
A:Accession: A93599  
A:Molecule type: mRNA  
A:Residues: 1-298 <SAT>  
A:Cross-references: GB:X03149; MID:g60997; PID:CAA26928.1; PID:g60998  
C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
C:Keywords: glycoprotein; transmembrane protein  
F:38-66/Domain: transmembrane #status predicted <TNM>  
F:85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 49; DB 1; Length 298;  
Best Local Similarity 100.0%; Pred. No. 3.9e-45;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGK 49  
|||||  
Db 149 KORQKPPSKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGK 197

RESULT 2  
JQ1205  
attachment protein - human respiratory syncytial virus (strain RSB1734)  
N:Alternate names: G protein  
C:Species: human respiratory syncytial virus  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Feb-1997

C:Accession: JQ1205  
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.  
J. Gen. Virol. 72, 2091-2096, 1991  
A:Title: Identification of variable domains of the attachment (G) protein of subgroup  
A:Reference number: JQ1204; MUID:91374005  
A:Accession: JQ1205  
A:Molecule type: mRNA  
A:Residues: 1-297 <CAN>  
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract  
infect and adults.  
C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
C:Keywords: glycoprotein; transmembrane protein  
F:85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 98.0%; Score 48; DB 2; Length 297;  
Best Local Similarity 100.0%; Pred. No. 4.5e-44;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KORQKPPSKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGK 48  
|||||  
Db 149 KORQKPPSKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGK 196

RESULT 3  
JQ1204  
attachment protein - human respiratory syncytial virus (strain RSB642)  
N:Alternate names: G protein  
C:Species: human respiratory syncytial virus  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Feb-1997  
C:Accession: JQ1204  
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.  
J. Gen. Virol. 72, 2091-2096, 1991  
A:Title: Identification of variable domains of the attachment (G) protein of subgroup  
A:Reference number: JQ1204; MUID:91374005  
A:Accession: JQ1204  
A:Molecule type: mRNA  
A:Residues: 1-297 <CAN>  
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract  
infect and adults.  
C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
C:Keywords: glycoprotein; transmembrane protein  
F:85,103,135,144,237,273/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.0%; Score 48; DB 2; Length 297;  
Best Local Similarity 100.0%; Pred. No. 4.5e-44;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGK 48  
|||||  
Db 149 KORQKPPSKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGK 196

RESULT 4  
JQ1208  
attachment protein - human respiratory syncytial virus (strain RSB6256)  
N:Alternate names: G protein  
C:Species: human respiratory syncytial virus  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Feb-1997  
C:Accession: JQ1208  
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.  
J. Gen. Virol. 72, 2091-2096, 1991  
A:Title: Identification of variable domains of the attachment (G) protein of subgroup  
A:Reference number: JQ1204; MUID:91374005  
A:Accession: JQ1208  
A:Molecule type: mRNA  
A:Residues: 1-297 <CAN>  
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract  
infect and adults.  
C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
C:Keywords: glycoprotein; transmembrane protein  
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status pred

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Query Match      81.6%; Score 40; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 197
|||||

RESULT 5
JC5680
G protein - Human respiratory syncytial virus
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1206
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1206
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
A:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract in
children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match      81.6%; Score 40; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 197
|||||

RESULT 6
MGNZRL
major surface glycoprotein G - human respiratory syncytial virus (strain Long)
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: A32703; S12279
R:Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A:Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and B
A:Reference number: A32703; MUID:87289657
A:Accession: A32703
A:Molecule type: mRNA
A:Residues: 1-298 <JOH>
A:Cross-references: GB:M17212; NID:g3333940; PIDN:AAA47411.1; PID:g3333941
R:Garcia-Barreno, B.; Portela, A.; Delgado, T.; Lopez, J.A.; Melero, J.A.
EMBO J. 9, 4181-4187, 1990
A:Title: Frame shift mutations as a novel mechanism for the generation of neutralization
A:Reference number: S12279; MUID:91065351
A:Accession: S12279
A:Molecule type: mRNA
A:Residues: 1-298 <GAR>
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:41-63/Domain: transmembrane #status predicted <TMN>
F:85,103,135,179,237,250,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status

Query Match      81.6%; Score 40; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 197
|||||

RESULT 9
JC5680
attachment protein - human respiratory syncytial virus (strain RSB5857)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1206
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1206
A:Molecule type: mRNA
A:Residues: 1-298 <CAN>
A:Experimental source: strain B79
A:Note: the authors translated the codon TTT for residue 165 and 170 as Glu, TTC for
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
F:1-38/Domain: intracellular #status predicted <INT>
F:39-66/Domain: transmembrane #status predicted <TMN>
F:67-298/Domain: extracellular #status predicted <EXC>

Query Match      81.6%; Score 40; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 158 KPNDHFHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 197
|||||

RESULT 8
JQ1209
attachment protein - human respiratory syncytial virus (strain RSB6614)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1209
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1209
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
A:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
er children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match      71.4%; Score 35; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 FHFEVFNPCSCSNNPTCWAICKRIPNKKPGKK 49
|||||
Db 163 FHFEVFNPCSCSNNPTCWAICKRIPNKKPGKK 197
|||||

RESULT 9
JQ1207
attachment protein - human respiratory syncytial virus (strain RSB6190)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1207
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
```

A:Title: Identification of variable domains of the attachment (G) protein of subgroup A  
A:Reference number: JQ1204; MUID:91374005  
A:Accession: JQ1207  
A:Molecule type: mRNA  
A:Residues: 1-298 <CAN>  
A>Note: The authors translated the codon ACC for residue 4 as Asn and AGC for residue 22  
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract ill-  
children and adults.  
C:Superfamily: respiratory syncytial virus-major surface glycoprotein G  
C:Keywords: glycoprotein; transmembrane protein  
F:85,103,135,237,250,273,294/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.3%; Score 33; DB 2; Length 298;  
Best Local Similarity 100.0%; Pred. No. 5.2e-28;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDPHEVFNPCSGCSNNPTCWAICKRIP 42  
|||||  
DB 158 KPNDPHEVFNPCSGCSNNPTCWAICKRIP 190  
|||||

RESULT 10  
MGNZ16  
major surface glycoprotein G - human respiratory syncytial virus (strain 18537)  
C:Species: human respiratory syncytial virus  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 16-Jul-1999  
C:Accession: B32703  
R:Johnson, P.R.; Striggs, M.K.; Olmsted, R.A.; Collins, P.L.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987  
A:Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and B:  
A:Reference number: A32703; MUID:87289657  
A:Accession: B32703  
A:Molecule type: mRNA  
A:Residues: 1-292 <JOH>  
A:Cross-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943  
C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
C:Keywords: glycoprotein; transmembrane protein  
F:41-63/Domain: transmembrane #status predicted <TMN>  
F:81,86,100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.5%; Score 13; DB 1; Length 292;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HFEVFNPCSC 28  
|||||  
DB 164 HFEVFNPCSC 176  
|||||

RESULT 11  
MGNZ60  
major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)  
N:Alternate names: attachment glycoprotein G  
C:Species: human respiratory syncytial virus  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Jul-1999  
C:Accession: A37077  
R:Sullender, W.M.; Anderson, K.; Wertz, G.W.  
Virology 178, 195-203, 1990  
A:Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis of  
gous subgroup virus challenge.  
A:Reference number: A37077; MUID:90357765  
A:Accession: A37077  
A:Molecule type: mRNA  
A:Residues: 1-292 <SUL>  
A:Cross-references: EMBL:M55633; NID:g333944; PIDN:AAA47413.1; PID:g333945  
C:Genetics:  
A:Gene: G  
C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
C:Keywords: glycoprotein; transmembrane protein  
F:45-63/Domain: transmembrane #status predicted <TMN>  
F:81,86,100,230,290/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.5%; Score 13; DB 1; Length 292;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HFEVFNPCSC 28  
|||||  
DB 164 HFEVFNPCSC 176  
|||||

RESULT 12  
B44213  
structural polyprotein - Venezuelan equine encephalitis virus (strain P676)  
N:Contains: 6K protein; coat protein; membrane glycoprotein E1; membrane glycoprotein  
C:Species: Venezuelan equine encephalitis virus  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 16-Jul-1999  
C:Accession: B44213  
R:Kinney, R.M.; Tsuchiya, K.R.; Snelder, J.M.; Trent, D.W.  
Virology 191, 569-580, 1992  
A:Title: Genetic evidence that epizootic Venezuelan equine encephalitis (VEE) viruses  
A:Reference number: A44213; MUID:93079859  
A:Accession: B44213  
A:Molecule type: genomic RNA  
A:Residues: 1-1255 <KIN>  
A:Cross-references: GB:L04653; NID:g290609; PIDN:AAC19319.1; PID:g290611  
C:Superfamily: togavirus structural polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-275/Product: coat protein #status predicted <CTP>  
F:276-334/Product: membrane glycoprotein E3 #status predicted <MG3>  
F:335-757/Product: membrane glycoprotein E2 #status predicted <MG2>  
F:702-722/Domain: transmembrane #status predicted <TM1>  
F:758-813/Product: 6K protein #status predicted <KP6>  
F:793-814/Domain: transmembrane #status predicted <TM2>  
F:814-1255/Product: membrane glycoprotein E1 #status predicted <MG1>  
F:1232-1249/Domain: transmembrane #status predicted <TM3>  
F:47,286,652,947/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 7; DB 1; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PNKPKGK 48  
|||||  
DB 108 PNKPKGK 114  
|||||

RESULT 13  
T05672  
hypothetical protein F22I13.210 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 23-Jul-1999  
C:Accession: T05672  
R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Meyers, H.W.; Mayer,  
submitted to the Protein Sequence Database, February 1999  
A:Reference number: 215420  
A:Accession: T05672  
A:Molecule type: DNA  
A:Residues: 1-1468 <BEV>  
A:Cross-references: EMBL:AL035539  
A:Experimental source: cultivar Columbia; BAC clone F22I13  
C:Genetics:  
A:Map position: 4  
A:Introns: 65/3; 346/1; 384/3; 440/2; 475/3; 562/3; 625/3; 1339/3; 1409/3  
A>Note: F22I13.210

Query Match 14.3%; Score 7; DB 2; Length 1468;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NKPPSKP 11

Db 32 NRPPSKP 38  
|||||||

## RESULT 14

D34047  
Stylar glycoprotein 7 - Persian tobacco (fragment)  
C:Species: Nicotiana glauca (Persian tobacco)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 13-Mar-1997  
C:Accession: D34047  
R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.  
Biochem. Biophys. Res. Commun. 166, 139-145, 1990  
A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage  
A:Reference number: A90157; MUID:90147691  
A:Accession: D34047  
A:Molecule type: protein  
A:Residues: 1-23 <JA4>  
C:Superfamily: Enterobacter ribonuclease  
C:Keywords: angiosperm reproduction; glycoprotein

Query Match 12.2%; Score 6; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 KRIPNK 44  
|||||||  
Db 17 KRIPNK 22

## RESULT 15

S69116  
fibrinogen gamma chain - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Mar-1998 #sequence\_revision 24-Apr-1998 #text\_change 02-Jul-1998  
C:Accession: S69116  
R:Ditvinovich, S.V.; Henschen, A.H.; Krieglstein, K.G.; Ingham, K.C.; Medved, L.V.  
Eur. J. Biochem. 229, 605-614, 1995  
A:Title: Structural and functional characterization of proteolytic fragments derived from  
A:Reference number: S69114; MUID:95278210  
A:Accession: S69116  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-92 <LIT>  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

Query Match 12.2%; Score 6; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PSKPNN 13  
|||||||  
Db 12 PSKPNN 17

Search completed: May 21, 2001, 14:18:17  
Job time: 95 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:17:57 ; Search time 8.3 seconds  
(without alignments)  
202.231 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 49

Sequence: 1 KORQKRPSPKPNDFEVEF.....NNPTCAICKRIPNKKPGKK 49

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	49	100.0	298	1 VGLG_HRSVA	P03423 human respi
2	48	98.0	297	1 VGLG_HRSV2	P27021 human respi
3	48	98.0	297	1 VGLG_HRSV3	P27022 human respi
4	40	81.6	297	1 VGLG_HRSV4	P27023 human respi
5	40	81.6	297	1 VGLG_HRSV6	P27025 human respi
6	40	81.6	298	1 VGLG_HRSVL	P20895 human respi
7	35	71.4	297	1 VGLG_HRSV7	P27026 human respi
8	33	67.3	298	1 VGLG_HRSV5	P27024 human respi
9	13	26.5	292	1 VGLG_HRSV1	P20896 human respi
10	13	26.5	292	1 VGLG_HRSV8	P23041 human respi
11	7	14.3	1255	1 POLS_EEVVP	P36332 venezuelan
12	6	12.2	126	1 RS13_STRCO	O86773 streptomyc
13	6	12.2	126	1 YO2L_CAEEL	P34671 caenorhabdi
14	6	12.2	159	1 RAC3_HUMAN	O14658 homo sapien
15	6	12.2	212	1 Y010_MYCPN	P75099 mycoplasma
16	6	12.2	218	1 Y010_MYCPE	P47256 mycoplasma
17	6	12.2	278	1 RT09_YEAST	P38120 saccharomyc
18	6	12.2	301	1 YAB4_SCHPO	O09806 schizosacch
19	6	12.2	413	1 IDHC_SOYBN	O06197 glycine max
20	6	12.2	444	1 FIBG_BOVIN	P12799 bos taurus
21	6	12.2	468	1 PCOL_RAT	O08628 rattus norv
22	6	12.2	508	1 SPAL_STAATU	P38507 staphylococ
23	6	12.2	524	1 SPAL_STAATU	P02976 staphylococ
24	6	12.2	544	1 SYFB_SULSO	P95960 sulfolobus
25	6	12.2	582	1 CIKG_HUMAN	O03721 homo sapien
26	6	12.2	615	1 COX1_BACP3	P16262 bacillus ps
27	6	12.2	625	1 CIKG_RAT	O63734 rattus norv
28	6	12.2	631	1 XRC1_MOUSE	Q60596 mus musculu
29	6	12.2	1254	1 POLS_EEVV8	P05674 venezuelan
30	6	12.2	1254	1 POLS_EEVVE	P36330 venezuelan
31	6	12.2	1254	1 POLS_EEVVM	P36331 venezuelan
32	6	12.2	1254	1 POLS_EEVVT	P09592 venezuelan
33	6	12.2	1255	1 POLS_EEVV3	P36329 venezuelan

34	6	12.2	1273	1 YAR2_SCHPO	Q10135 schizosacch
35	6	12.2	1651	1 VIT6_CAEEL	P18948 caenorhabdi
36	6	12.2	1896	1 RPB1_DROME	P04052 drosophila
37	5	10.2	74	1 SOK_ECOLI	P13971 escherichia
38	5	10.2	75	1 ULL1_EBV	P03216 Epstein-bar
39	5	10.2	94	1 IHFB_BUCAI	P57394 buchnera ap
40	5	10.2	96	1 XYO1_HUMAN	P23262 homo sapien
41	5	10.2	101	1 FXC2_RAT	Q63246 mus musculu
42	5	10.2	103	1 CHLB_LYCAN	P37847 lycopodium
43	5	10.2	103	1 CHLB_LYCCO	P37848 lycopodium
44	5	10.2	103	1 CHLB_SELMO	P37856 selaginella
45	5	10.2	104	1 RL36_CAEEL	P49181 caenorhabdi
46	5	10.2	112	1 SPAM_SHIFL	P49108 shigella fl
47	5	10.2	116	1 GLHA_ICTGU	P53542 clarifas gar
48	5	10.2	116	1 GLHA_ICTPU	Q9Y9P3 ictalurus p
49	5	10.2	120	1 VP3_CAV26	P54095 chicken ane
50	5	10.2	121	1 VP3_CAV82	P54096 chicken ane
51	5	10.2	121	1 VP3_CAVC1	Q99132 chicken ane
52	5	10.2	121	1 VP3_CAVC1	P54094 chicken ane
53	5	10.2	125	1 ACPS_ECOLI	P24224 escherichia
54	5	10.2	125	1 YCXL_GUTHH	O78420 guillardia
55	5	10.2	136	1 Y16K_CSMV	P18919 chloris str
56	5	10.2	144	1 YV05_METJA	O60304 methanococ
57	5	10.2	147	1 NIFU_BACSU	O32163 bacillus su
58	5	10.2	151	1 UBC2_NEUCR	P52493 neurospora
59	5	10.2	158	1 YS31_CAEEL	Q09368 caenorhabdi
60	5	10.2	159	1 RS11_MAIZE	P25460 zea mays (m
61	5	10.2	160	1 E13J_TOBAC	P52397 nicotiana t
62	5	10.2	173	1 PRL_MEDFR	O40374 medicago tr
63	5	10.2	180	1 PAAD_THERAC	Q9HJ72 thermoplas
64	5	10.2	180	1 Y16A_MYCFU	Q02039 mycoplasma
65	5	10.2	182	1 PAAD_ARCFU	Q29054 archaeoglob
66	5	10.2	190	1 GCH1_CAMJE	P51594 campylobact
67	5	10.2	191	1 LEUD_LACLA	Q02144 lactococcus
68	5	10.2	194	1 YQ03_CAEEL	Q09294 caenorhabdi
69	5	10.2	196	1 YEL9_YEAST	P40018 saccharomyc
70	5	10.2	198	1 RECR_STRPN	Q9ZHC4 streptococ
71	5	10.2	200	1 SYST_LYCES	P27058 lycopersico
72	5	10.2	201	1 YADL_ECOLI	P37017 escherichia
73	5	10.2	202	1 NUKM_TRYBB	Q26783 trypanosoma
74	5	10.2	203	1 RB13_HUMAN	P51153 homo sapien
75	5	10.2	204	1 IPP2_RABIT	P11845 oryctolagus
76	5	10.2	205	1 POLG_CXA23	P08490 coxsackievi
77	5	10.2	205	1 YICG_ECOLI	P31432 escherichia
78	5	10.2	206	1 YCX1_CYAPA	P48323 cyanophora
79	5	10.2	209	1 YIL3_YEAST	P40479 saccharomyc
80	5	10.2	211	1 YFDX_ECOLI	P76520 escherichia
81	5	10.2	213	1 GBI_MEDSA	P30286 medicago sa
82	5	10.2	213	1 GCHI_OSTOS	O61573 ostertagia
83	5	10.2	213	1 RB25_HUMAN	P57735 homo sapien
84	5	10.2	217	1 H1_ANAPL	P09426 anas platyr
85	5	10.2	217	1 H1_CHICK	P09987 gallus gall
86	5	10.2	218	1 H101_CHICK	P08284 gallus gall
87	5	10.2	219	1 YB87_ARATH	O81004 arabidopsis
88	5	10.2	219	1 YOFA_ECOLI	Q46827 escherichia
89	5	10.2	220	1 FGF3_CHICK	P48801 gallus gall
90	5	10.2	223	1 GCHI_CAEEL	Q19980 caenorhabdi
91	5	10.2	224	1 T2V1_BACST	P43421 bacillus st
92	5	10.2	225	1 RU2B_HUMAN	P08579 homo sapien
93	5	10.2	225	1 TPIS_PYRMO	P95583 pyrococcus
94	5	10.2	229	1 NISR_LACLA	Q07597 lactococcus
95	5	10.2	229	1 VIF_CAEVC	P33462 caprine art
96	5	10.2	229	1 VV_PI4HA	P21739 human parai
97	5	10.2	229	1 Y467_BORBU	O51423 borrelia bu
98	5	10.2	231	1 TPIS_PYRHO	O59536 pyrococcus
99	5	10.2	235	1 C554_NITEU	Q37142 nitrosomona
100	5	10.2	236	1 CD81_CERAE	P37703 cercopithe
101	5	10.2	236	1 CD81_HUMAN	P18582 homo sapien
102	5	10.2	236	1 CD81_MOUSE	P35762 mus musculu
103	5	10.2	236	1 CD81_RAT	Q62745 rattus norv
104	5	10.2	238	1 ET3_HUMAN	P14138 homo sapien
105	5	10.2	243	1 GCHI_YEAST	P51601 saccharomyc
106	5	10.2	246	1 RS3_DROME	Q06559 drosophila

107	5	10.2	247	1	MCT1_HUMAN	P23946	homo sapien	180	379	1	5H1D_FUGRU	P79748	fugu rubrip
108	5	10.2	247	1	MCT1_MACFA	P56435	macaca fasc	181	379	1	CYBA_STELO	P24962	stenella lo
109	5	10.2	247	1	MCT1_PAPHA	P52195	papio hamad	182	379	1	CYBB_STELO	P24963	stenella lo
110	5	10.2	249	1	MCT1_CANFA	P21842	canis famil	183	379	1	CYB_ALCAA	O47922	alces alces
111	5	10.2	251	1	Y4EF_RHSN	P55429	rhibobium s	184	379	1	CYB_AMMLE	O78781	ammotragus
112	5	10.2	253	1	SA0B_CHITE	Q05019	chironomus	185	379	1	CYB_ANTAM	P24992	antilocapra
113	5	10.2	253	1	VG23_HSVSA	Q01006	herpesvirus	186	379	1	CYB_ARTAD	O95719	artibeus an
114	5	10.2	260	1	NADE_HELPJ	Q92mb0	helicobacte	187	379	1	CYB_ARTAZ	O95718	artibeus an
115	5	10.2	260	1	NADE_HELPJ	O25096	helicobacte	188	379	1	CYB_ARTCI	Q95726	artibeus ci
116	5	10.2	268	1	SET_DROME	P53997	drosophila	189	379	1	CYB_ARTFI	Q95723	artibeus co
117	5	10.2	270	1	YKAA_CAEEL	P18346	equine herp	190	379	1	CYB_ARTFI	Q95728	artibeus fi
118	5	10.2	273	1	IE68_HSVEA	P24887	caenorhabdi	191	379	1	CYB_ARTFR	O95727	artibeus fr
119	5	10.2	275	1	E131_TOBAC	P27792	mus musculu	192	379	1	CYB_ARTGA	O95731	artibeus gl
120	5	10.2	278	1	LX1L_MOUSE	O67693	aquifex aeo	193	379	1	CYB_ARTGG	O95729	artibeus gl
121	5	10.2	279	1	DAPE_AQUAE	Q61470	mus musculu	194	379	1	CYB_ARTGW	Q95730	artibeus gl
122	5	10.2	281	1	CD37_MOUSE	P31053	rattus norv	195	379	1	CYB_ARTHA	Q95734	artibeus ha
123	5	10.2	281	1	CD37_MOUSE	P15643	klebsiella	196	379	1	CYB_ARTHI	Q95735	artibeus hi
124	5	10.2	285	1	GSPC_KLEPN	P07182	drosophila	197	379	1	CYB_ARTIO	Q95737	artibeus in
125	5	10.2	286	1	CH36_DROME	P24887	caenorhabdi	198	379	1	CYB_ARTIT	Q95736	artibeus in
126	5	10.2	291	1	NU1M_CAEEL	P45208	haemophilus	199	379	1	CYB_ARTJA	O95738	artibeus ja
127	5	10.2	292	1	METF_HAEIN	Q9p4c1	kluyveromyc	200	379	1	CYB_ARTLI	Q95739	artibeus li
128	5	10.2	292	1	RT09_KLUMA	P54000	saccharomyc	201	379	1	CYB_ARTOB	Q95741	artibeus ob
129	5	10.2	292	1	SUB1_YEAST	P17111	drosophila	202	379	1	CYB_ARTPH	Q95744	artibeus ph
130	5	10.2	293	1	CH36_DROVI	P14300	rhodospiril	203	379	1	CYB_ARTPL	Q95745	artibeus pl
131	5	10.2	294	1	DRAG_RHORI	Q9xt56	bos taurus	204	379	1	CYB_ARTPL	Q95750	artibeus to
132	5	10.2	298	1	JAMI_BOVIN	O9V624	homo sapien	205	379	1	CYB_ASTPE	Q33818	asterina pe
133	5	10.2	299	1	JAMI_HUMAN	P28907	homo sapien	206	379	1	CYB_BALAC	P41280	balaeonopter
134	5	10.2	300	1	CD38_HUMAN	O88792	homo sapien	207	379	1	CYB_BALBN	P41281	balaeonopter
135	5	10.2	300	1	JAMI_MOUSE	P20180	cowpea chlo	208	379	1	CYB_BALBO	P41282	balaeonopter
136	5	10.2	302	1	MOVP_CCMV	P24139	bacillus su	209	379	1	CYB_BALGL	P41283	balaeonopter
137	5	10.2	305	1	OPPC_BACSU	P47129	saccharomyc	210	379	1	CYB_BALGL	P41284	balaeonopt
138	5	10.2	309	1	YJ53_YEAST	P76049	escherichia	211	379	1	CYB_BALMU	P41285	balaeonopt
139	5	10.2	310	1	YCJY_ECOLI	P32129	escherichia	212	379	1	CYB_BALMY	P41286	balaeonopt
140	5	10.2	310	1	YIHG_ECOLI	P06548	bacillus ce	213	379	1	CYB_BALPH	P41286	balaeonopt
141	5	10.2	316	1	BLA3_BACCE	O99795	homo sapien	214	379	1	CYB_BEAHU	P24950	balaeonopter
142	5	10.2	319	1	A33_HUMAN	Q50290	mycoplasma	215	379	1	CYB_BOVIN	O47420	beatragus h
143	5	10.2	319	1	YB38_MYCPN	P17110	ceratitis c	216	379	1	CYB_CAMBA	P00157	bos taurus
144	5	10.2	320	1	CH36_CERCA	Q09377	caenorhabdi	217	379	1	CYB_CAMDR	Q34028	camelus bac
145	5	10.2	322	1	Y553_CAEEL	P04579	mycobacteri	218	379	1	CYB_CAPAE	P24952	camelus dro
146	5	10.2	323	1	Y495_MYCLE	P07739	vibrio harv	219	379	1	CYB_CAPCU	O78788	capra cauca
147	5	10.2	324	1	LUXB_VIBHA	P42975	bacillus su	220	379	1	CYB_CAPCY	O78787	capra cylin
148	5	10.2	325	1	BIRA_BACSU	P47976	saccharomyc	221	379	1	CYB_CAPHI	O78786	capra falco
149	5	10.2	325	1	CTH1_YEAST	O30620	mycobacteri	222	379	1	CYB_CAPIB	P24953	capra hircu
150	5	10.2	325	1	MODD_MYCBO	Q50906	mycobacteri	223	379	1	CYB_CAPIB	O78785	capra ibex
151	5	10.2	325	1	MODD_MYCBO	Q91rdv6	mycoplasma	224	379	1	CYB_CAPNR	P41287	caperea mar
152	5	10.2	325	1	RPOA_MYCTU	P52398	nicotiana t	225	379	1	CYB_CAPNU	O78790	capra nubia
153	5	10.2	331	1	E13K_TOBAC	O09203	caenorhabdi	226	379	1	CYB_CAPPY	O47926	capreolus p
154	5	10.2	331	1	SRA1_CAEEL	P29888	vaccinia vi	227	379	1	CYB_CEREL	O47924	cervus elap
155	5	10.2	331	1	Y244_METJA	P60299	methanococc	228	379	1	CYB_CERNI	Q34172	cervus nipp
156	5	10.2	333	1	OAC_BPSF6	P23214	bacterioph	229	379	1	CYB_CONTA	O47421	connochaete
157	5	10.2	336	1	RF09_CANAL	O94150	candida alb	230	379	1	CYB_DAMDA	P24955	dama dama
158	5	10.2	337	1	VF11_VACCP	P29888	vaccinia vi	231	379	1	CYB_DASNO	O21337	dasyptus nov
159	5	10.2	338	1	RFPG_HAEIN	P44914	haemophilus	232	379	1	CYB_DELEL	Q03812	deiphinapte
160	5	10.2	343	1	E13G_TOBAC	P23547	nicotiana t	233	379	1	CYB_DUGDU	Q33401	dugong dugo
161	5	10.2	347	1	TOLA_PSEAE	P50600	pseudomonas	234	379	1	CYB_ERIEU	Q36368	erinaeace e
162	5	10.2	347	1	YDJJ_ECOLI	P77280	escherichia	235	379	1	CYB_ESCGI	P41288	eschrictiit
163	5	10.2	350	1	NTRB_VIBAL	P19906	vibrio algi	236	379	1	CYB_GAZGA	O48336	gazella gaz
164	5	10.2	351	1	CAV2_CAEEL	Q18879	caenorhabdi	237	379	1	CYB_HEMJE	O78783	hemitraque
165	5	10.2	351	1	P53_ORYLA	P79820	oryzias lat	238	379	1	CYB_HYDLN	O47930	hydropotes
166	5	10.2	356	1	E13L_TOBAC	P52399	nicotiana t	239	379	1	CYB_LAMGL	Q34891	lama glama
167	5	10.2	357	1	TGN3_RAT	P19814	rattus norv	240	379	1	CYB_LAMPA	Q34916	lama guanic
168	5	10.2	358	1	Y502_MYCTU	Q11167	mycobacteri	241	379	1	CYB_LAMVI	Q36227	lama vicugn
169	5	10.2	359	1	ALF_BORBU	O51401	borrelia bu	242	379	1	CYB_MEGNO	P41289	megaptera n
170	5	10.2	361	1	HEM3_HUMAN	P22907	homo sapien	243	379	1	CYB_MONMO	P92657	monodon mon
171	5	10.2	361	1	HEM3_MOUSE	P08397	homo sapien	244	379	1	CYB_MOSLE	O47584	moschus leu
172	5	10.2	367	1	HEM3_RAT	P19356	rattus norv	245	379	1	CYB_MOSMO	P24960	moschus mos
173	5	10.2	367	1	Y502_MYCLE	P54878	mycobacteri	246	379	1	CYB_ODOHO	Q95753	odocoileus
174	5	10.2	368	1	TRPC_ARATH	P49572	arabidopsis	247	379	1	CYB_OVIDA	O78778	ovis ammon
175	5	10.2	370	1	P2C2_SCHPO	Q09172	schizosacch	248	379	1	CYB_OVIDA	O78779	ovis dalli
176	5	10.2	372	1	AG1_LURDI	P11218	urtica dioi	249	379	1	CYB_OVIVI	O78780	ovis vignei
177	5	10.2	373	1	GLNA_MOUSE	P15105	mus musculu	250	379	1	CYB_PHOGR	Q35457	phoca groen
178	5	10.2	376	1	KDCB_DROME	P16911	drosophila	251	379	1	CYB_PHOPH	O03811	phocaenoide
179	5	10.2	378	1	BI0B_ARATH	P54967	arabidopsis	252	379	1			

253 10.2 379 1 CYB\_PHYCA P41290 physeter ca  
254 5 10.2 379 1 CYB\_PIG P24964 sus scrofa  
255 5 10.2 379 1 CYB\_PSENA O78782 pseudoris na  
256 5 10.2 379 1 CYB\_RABIT P34863 oryctolagus  
257 5 10.2 379 1 CYB\_SHEEP P24959 ovis aries  
258 5 10.2 379 1 CYB\_SIGLI O47419 sigmocerops  
259 5 10.2 379 1 CYB\_STEAT P24961 stenella at  
260 5 10.2 379 1 CYB\_TAYTA P24966 tayassu taj  
261 5 10.2 379 1 CYB\_TRANA P24965 tragulus na  
262 5 10.2 380 1 COAT\_CNV P15183 cucumber ne  
263 5 10.2 380 1 CYB\_ACITR P11669 acipenser t  
264 5 10.2 380 1 CYB\_CAPSI O78784 capra sibir  
265 5 10.2 380 1 CYB\_GADMO O78080 gadus morhu  
266 5 10.2 380 1 CYB\_LATCH O03176 latimeria c  
267 5 10.2 380 1 CYB\_MICAR Q36922 microtus ar  
268 5 10.2 380 1 CYB\_MICLO P56731 microtus lo  
269 5 10.2 380 1 CYB\_PELSU O79680 pelomedusa  
270 5 10.2 380 1 CYB\_RAT P00159 rattus norv  
271 5 10.2 380 1 CYB\_RUPPY O78777 rupicapra p  
272 5 10.2 381 1 CYB\_ANTLR O63537 antechinus  
273 5 10.2 381 1 CYB\_ANTA Q33800 antechinus  
274 5 10.2 381 1 CYB\_DASRO Q34376 dasykaluta  
275 5 10.2 381 1 CYB\_MOUSE P00158 mus musculu  
276 5 10.2 381 1 CYB\_MURLO Q35020 murexia lon  
277 5 10.2 381 1 CYB\_MYOME Q35038 myoictis me  
278 5 10.2 382 1 CYB\_MONDO Q04911 monodelphis  
279 5 10.2 383 1 TRML\_PYRAB Q9vlp3 pyrococcus  
280 5 10.2 385 1 CYB\_SACDO Q35819 saccharomyc  
281 5 10.2 385 1 CYB\_YEAST P00163 saccharomyc  
282 5 10.2 396 1 Q45E\_DROME Q9v589 drosophila  
283 5 10.2 397 1 YKRP\_CAEEL P34303 caenorhabdi  
284 5 10.2 399 1 RRPP\_PI4HA P22044 human parai  
285 5 10.2 402 1 YJT3\_YEAST P39542 saccharomyc  
286 5 10.2 405 1 YLF2\_YEAST P38746 saccharomyc  
287 5 10.2 411 1 YAL2\_SCHPO Q09685 schizosacch  
288 5 10.2 413 1 CRF2\_XENIA Q42603 xenopus lae  
289 5 10.2 416 1 CREA\_EMENI Q01981 emeritella  
290 5 10.2 419 1 CLPX\_CHLTR O84711 chlamydia t  
291 5 10.2 420 1 CAQS\_RANES P31231 rana esculu  
292 5 10.2 420 1 GLYA\_ACTAC P43844 haemophilus  
293 5 10.2 421 1 GLYA\_HAETN Q58916 methanococc  
294 5 10.2 422 1 YF2L\_MERJA P22051 tomato blac  
295 5 10.2 424 1 V54E\_TBRSV Q05620 aspergillus  
296 5 10.2 427 1 CREA\_ASPNG P46277 medicago va  
297 5 10.2 428 1 CG1B\_MEDVA Q94166 aspergillus  
298 5 10.2 431 1 CREA\_ASPAC Q10223 schizosacch  
299 5 10.2 431 1 YAZL\_SCHPO Q04723 lactococcus  
300 5 10.2 435 1 PEPC\_LACLC Q23085 heterodontu  
301 5 10.2 438 1 HVC2\_HETFR Q43365 homo sapien  
302 5 10.2 443 1 HXA3\_HUMAN P23790 xenopus lae  
303 5 10.2 448 1 SRF\_XENIA P10063 bos taurus  
304 5 10.2 451 1 GAA2\_BOVIN P47869 homo sapien  
305 5 10.2 451 1 GAA2\_HUMAN P26048 mus musculu  
306 5 10.2 451 1 GAA2\_MOUSE P23576 rattus norv  
307 5 10.2 451 1 GAA2\_RAT P52715 caenorhabdi  
308 5 10.2 454 1 YUA6\_CAEEL Q02819 mus musculu  
309 5 10.2 455 1 NCBI\_MOUSE P29315 rattus norv  
310 5 10.2 456 1 RINI\_RAT Q03648 saccharomyc  
311 5 10.2 457 1 YM59\_YEAST Q9ze58 rickettsia  
312 5 10.2 461 1 KDTA\_RICPR P24057 anas platyr  
313 5 10.2 466 1 CRD1\_ANAPL P33110 anser anser  
314 5 10.2 466 1 CRD1\_ANANP P24058 anas platyr  
315 5 10.2 468 1 CRD2\_ANAPL Q09270 brachydanio  
316 5 10.2 472 1 POU2\_BRARE Q233525 caenorhabdi  
317 5 10.2 472 1 YWIE\_CAEEL Q33126 balanus amp  
318 5 10.2 476 1 GREI\_BALAM P46997 saccharomyc  
319 5 10.2 482 1 YJQ2\_YEAST P47376 mycoplasma  
320 5 10.2 484 1 Y130\_MYCGE Q01447 fusarium so  
321 5 10.2 485 1 ER24\_FUSSO Q35367 homo sapien  
322 5 10.2 487 1 HH1R\_HUMAN P70174 mus musculu  
323 5 10.2 488 1 HH1R\_MOUSE P30546 bos taurus  
324 5 10.2 491 1 HH1R\_BOVIN O70475 mus musculu  
325 5 10.2 493 1 UGDH\_MOUSE

326 5 10.2 493 1 UGDH\_RAT O70199 rattus norv  
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328 5 10.2 494 1 UGDH\_BOVIN P23738 bos taurus  
329 5 10.2 494 1 UGDH\_HUMAN O60701 homo sapien  
330 5 10.2 496 1 NIFE\_RHISN P55673 rhizobium s  
331 5 10.2 496 1 NOS2\_RABIT O19114 oryctolagus  
332 5 10.2 498 1 IL14\_HUMAN P40222 homo sapien  
333 5 10.2 501 1 FXC2\_HUMAN Q99958 homo sapien  
334 5 10.2 501 1 LCYB\_ARATH Q38933 arabidopsis  
335 5 10.2 503 1 NRFL\_MOUSE Q16656 homo sapien  
336 5 10.2 503 1 NRFL\_MOUSE Q9u000 mus musculu  
337 5 10.2 504 1 ENGA\_HAETN P44536 haemophilus  
338 5 10.2 504 1 Y4JA\_RHISN P55501 rhizobium s  
339 5 10.2 506 1 UDPG\_SCHPO P78811 schizosacch  
340 5 10.2 507 1 CHLB\_PORPU P51278 porphyra pu  
341 5 10.2 508 1 CROC\_DROME P32027 drosophila  
342 5 10.2 508 1 SRF\_HUMAN P11831 homo sapien  
343 5 10.2 508 1 VLI\_HPVS6 P50821 human papil  
344 5 10.2 509 1 Y736\_HAETN P44849 haemophilus  
345 5 10.2 509 1 C4AI\_DROME Q9vms9 drosophila  
346 5 10.2 509 1 DHAC\_CHICK P27463 gallus gall  
347 5 10.2 510 1 ATPA\_BUCAP O51874 buchera ap  
348 5 10.2 512 1 ATPA\_BUCAI P57122 buchera ap  
349 5 10.2 517 1 Z215\_HUMAN Q9u158 homo sapien  
350 5 10.2 518 1 PR31\_SCHPO Q42504 schizosacch  
351 5 10.2 526 1 HRG\_RABIT Q28640 oryctolagus  
352 5 10.2 527 1 YEGH\_ECOLI P76389 escherichia  
353 5 10.2 529 1 IMA2\_HUMAN P52292 homo sapien  
354 5 10.2 537 1 TEE6\_STRPY P18481 streptococc  
355 5 10.2 540 1 YMA5\_CAEEL P34450 caenorhabdi  
356 5 10.2 541 1 PRPR\_SALTY P74839 salmonella  
357 5 10.2 544 1 AGMI\_CANAL Q9p4v2 candida alb  
358 5 10.2 550 1 YL00\_MYCTU Q10709 mycobacteri  
359 5 10.2 553 1 FXCL\_HUMAN Q12948 homo sapien  
360 5 10.2 553 1 FXCL\_MOUSE Q12948 homo sapien  
361 5 10.2 556 1 PPBD\_BACSU Q61572 mus musculu  
362 5 10.2 561 1 YGG4\_YEAST P42251 bacillus su  
363 5 10.2 565 1 VNUC\_INCCA P3166 saccharomyc  
364 5 10.2 566 1 Y397\_MYCGE P08028 influenza c  
365 5 10.2 577 1 G6PC\_SOLTU P7637 mycoplasma  
366 5 10.2 582 1 TNPA\_BACFR Q43839 solanum tub  
367 5 10.2 585 1 ASNI\_LOTJA Q45119 bacteroides  
368 5 10.2 585 1 ASNI\_PEA P49092 lotus japon  
369 5 10.2 585 1 YAOH\_SCHPO P19251 pisum sativ  
370 5 10.2 587 1 NDC2\_RAT Q10096 schizosacch  
371 5 10.2 589 1 ASNS\_ASPOF P70545 rattus norv  
372 5 10.2 592 1 NDC1\_HUMAN P31752 asparagus o  
373 5 10.2 603 1 SNTD\_HAETN Q13183 homo sapien  
374 5 10.2 605 1 RTK2\_GEOCY P44569 haemophilus  
375 5 10.2 609 1 HSF\_SCHPO P42159 geodia cydo  
376 5 10.2 610 1 CDP1\_ARATH Q02953 schizosacch  
377 5 10.2 619 1 M3K2\_MOUSE Q06850 arabidopsis  
378 5 10.2 622 1 YAE7\_YEAST Q61083 mus musculu  
379 5 10.2 623 1 NRC2\_NEUCR P39723 saccharomyc  
380 5 10.2 628 1 DP19\_CAEEL Q42626 neurospora  
381 5 10.2 632 1 FMN2\_HUMAN P34413 caenorhabdi  
382 5 10.2 639 1 NRG1\_HUMAN Q9nz56 homo sapien  
383 5 10.2 644 1 YED0\_YEAST Q02297 h pro-neure  
384 5 10.2 648 1 PIG1\_YEAST P39987 saccharomyc  
385 5 10.2 654 1 PSTA\_MYCGE Q06216 saccharomyc  
386 5 10.2 662 1 NRG1\_RAT P47651 mycoplasma  
387 5 10.2 667 1 KJF7\_YEAST P43322 r pro-neure  
388 5 10.2 674 1 TML1\_ARATH P47042 saccharomyc  
389 5 10.2 682 1 YB89\_METJA P33543 arabidopsis  
390 5 10.2 687 1 VS41\_GIALA Q58884 methanococc  
391 5 10.2 688 1 CHLB\_CHLRE P92127 giardia lam  
392 5 10.2 689 1 GALX\_PACTA P36437 chlamydomon  
393 5 10.2 689 1 YQ2\_HELPY P40801 pachysolen  
394 5 10.2 691 1 PP21\_YEAST P56185 helicobacte  
395 5 10.2 692 1 YB30\_HELPJ P26570 saccharomyc  
396 5 10.2 697 1 Y441\_HUMAN Q9zj16 helicobacte  
397 5 10.2 702 1 ADA3\_YEAST Q43167 homo sapien  
398 5 10.2 704 1 CDGT\_BACOH P32494 saccharomyc  
399 5 10.2 704 1 CDGT\_BACOH P27036 bacillus oh

399	5	10.2	707	1	SFPQ_HUMAN	P23246	homo sapien	472	5	10.2	1221	1	UBP2_KLULIA	O42726	kluyveromyc
400	5	10.2	710	1	CDGT_THETU	P26827	thermoanaer	473	5	10.2	1230	1	ST20_CANAL	Q92312	candida alb
401	5	10.2	715	1	VGL_SVP1	P15892	spiroplasma	474	5	10.2	1253	1	POLS_SFV	Q33315	semliki for
402	5	10.2	718	1	CDGT_BACCI	P30920	bacillus ci	475	5	10.2	1270	1	DYNA_HUMAN	Q14203	homo sapien
403	5	10.2	718	1	CDGT_BACCI	P14014	bacillus li	476	5	10.2	1270	1	DYNA_HUMAN	Q01476	saccharomyc
404	5	10.2	718	1	CDGT_BACCI	P31747	bacillus sp	477	5	10.2	1280	1	DYNA_RAT	P28023	rattus norv
405	5	10.2	722	1	Y174_RICPR	P81171	rickettsia	478	5	10.2	1281	1	DYNA_MOUSE	O08788	mus musculus
406	5	10.2	746	1	EXTL_HUMAN	Q16394	homo sapien	479	5	10.2	1321	1	YAG3_YEAST	P39712	saccharomyc
407	5	10.2	746	1	EXTL_MOUSE	P97464	mus musculus	480	5	10.2	1328	1	POLX_TOBAC	P10978	nicotiana t
408	5	10.2	773	1	ITB1_BOVIN	P53712	bos taurus	481	5	10.2	1328	1	KAB7_YEAST	P31374	saccharomyc
409	5	10.2	788	1	ACON_CAEEL	P34455	caenorhabdi	482	5	10.2	1380	1	ZMS1_YEAST	P46974	saccharomyc
410	5	10.2	793	1	S3A1_HUMAN	P15459	homo sapien	483	5	10.2	1390	1	INSR_AEDAE	Q93105	aedes aegypt
411	5	10.2	798	1	ITB0_XENLA	P12607	xenopus lae	484	5	10.2	1405	1	RPL1_SCHPO	O94666	schizosacch
412	5	10.2	798	1	ITB1_FELCA	P53713	felis silve	485	5	10.2	1419	1	MDR_PLAFA	P13568	plasmodium
413	5	10.2	798	1	ITB1_HUMAN	P05556	homo sapien	486	5	10.2	1468	1	DPOA_YEAST	P13382	saccharomyc
414	5	10.2	798	1	ITB1_MOUSE	P09055	mus musculus	487	5	10.2	1471	1	MYS4_YEAST	P32492	saccharomyc
415	5	10.2	798	1	ITB1_XENLA	P12606	xenopus lae	488	5	10.2	1471	1	HTK7_HYDAT	Q25197	hydra atten
416	5	10.2	799	1	ITB1_RAT	P49134	rattus norv	489	5	10.2	1492	1	DPOA_OXNO	Q94636	oxytricha n
417	5	10.2	803	1	ITB1_CHICK	P07228	gallus gall	490	5	10.2	1508	1	AT5A_MOUSE	O54827	mus muscula
418	5	10.2	803	1	UBPE_YEAST	P38237	saccharomyc	491	5	10.2	1513	1	DPOA_OXTR	Q27152	oxytricha t
419	5	10.2	817	1	YGAB_YEAST	P46951	saccharomyc	492	5	10.2	1525	1	POLG_STEVM	P09732	st. louis e
420	5	10.2	834	1	ALIM_YEAST	P03875	saccharomyc	493	5	10.2	1570	1	P3K1_DICDI	P54673	dictyosteli
421	5	10.2	851	1	ENV_HVZDI	P17755	human immun	494	5	10.2	1603	1	VIT5_CAEEL	P06125	caenorhabdi
422	5	10.2	865	1	TOPI_ECOLI	P06612	escherichia	495	5	10.2	1629	1	RRPO_SHMV	P83202	sunn-hemp m
423	5	10.2	880	1	SVF_BACST	P11931	bacillus st	496	5	10.2	1700	1	BAR3_CHITE	Q03376	chironomus
424	5	10.2	886	1	SUHW_DROAN	Q08875	drosophila	497	5	10.2	1772	1	MSPI_PLAYO	P13828	plasmodium
425	5	10.2	899	1	SUHW_DROVI	Q08876	drosophila	498	5	10.2	1873	1	CCAS_RABIT	P07293	oryctolagus
426	5	10.2	907	1	TREA_CANAL	P52494	candida alb	499	5	10.2	1906	1	KMLS_CHICK	P11799	gallus gall
427	5	10.2	917	1	MSH2_DROME	P43248	drosophila	500	5	10.2	1914	1	KMLS_HUMAN	O60318	homo sapien
428	5	10.2	918	1	IL6B_RAT	P40190	rattus norv	501	5	10.2	1980	1	MC3A_HUMAN	O97159	drosophila
429	5	10.2	919	1	YK05_YEAST	P36051	saccharomyc	502	5	10.2	2136	1	YCF2_MARPO	P09975	marichantia
430	5	10.2	923	1	RE11_SCHPO	Q92380	schizosacch	503	5	10.2	2203	1	POLG_EC09B	O66577	e genome po
431	5	10.2	927	1	IF2_STRAG	O9420	streptococc	504	5	10.2	2206	1	POLG_CXA21	P22055	c genome po
432	5	10.2	937	1	MSH2_NEUCR	O13396	neurospora	505	5	10.2	2206	1	POLG_POLIM	P03299	p genome po
433	5	10.2	944	1	SUHW_DROME	P08970	drosophila	506	5	10.2	2208	1	POLH_POLIM	P03300	p genome po
434	5	10.2	945	1	SVF_NEIMA	Q91x22	neisseria m	507	5	10.2	2209	1	POLG_POLIS	P03301	poliovirus
435	5	10.2	945	1	SVF_NEIMB	Q9K1h7	neisseria m	508	5	10.2	2214	1	POLG_CXA24	P36290	c genome po
436	5	10.2	950	1	Y136_HUMAN	Q14149	homo sapien	509	5	10.2	2294	1	YCF2_ARATH	P56786	arabidopsis
437	5	10.2	950	1	Y311_RICPR	Q92d36	rickettsia	510	5	10.2	2295	1	WDR9_HUMAN	Q9ns16	homo sapien
438	5	10.2	952	1	YK15_CAEEL	P46012	caenorhabdi	511	5	10.2	2301	1	POLG_TMEVD	P13899	t genome po
439	5	10.2	959	1	MSH1_YEAST	P25846	saccharomyc	512	5	10.2	2303	1	POLG_TMEVB	P08544	t genome po
440	5	10.2	964	1	UL70_MCMVS	Q99153	murine cyto	513	5	10.2	2303	1	POLG_TMEVG	P08545	t genome po
441	5	10.2	970	1	S0U1_YEAST	P33550	saccharomyc	514	5	10.2	2375	1	ATRX_HUMAN	P46100	homo sapien
442	5	10.2	976	1	PD33_YEAST	P33200	saccharomyc	515	5	10.2	2555	1	PPS3_BACSU	P39847	bacillus su
443	5	10.2	996	1	PIP2_YEAST	P52960	saccharomyc	516	5	10.2	3063	1	CA1C_HUMAN	Q99715	homo sapien
444	5	10.2	996	1	VGNM_RCMV	P13561	red clover	517	5	10.2	3067	1	CA1C_MOUSE	Q60847	mus musculu
445	5	10.2	1001	1	IF2_SYNY3	P22689	synecocyst	518	5	10.2	3176	1	CA36_HUMAN	P12111	homo sapien
446	5	10.2	1002	1	SVIM_YEAST	P48526	saccharomyc	519	5	10.2	3655	1	YAMB_SCHPO	Q10064	schizosacch
447	5	10.2	1036	1	YAN2_SCHPO	Q10068	schizosacch	520	5	10.2	3726	1	TRX_DROME	P20659	drosophila
448	5	10.2	1051	1	CARB_SULSO	Q59969	sulfolobus	521	5	10.2	4660	1	LRP2_RAT	P98158	rattus norv
449	5	10.2	1052	1	MGPC_MYCCE	P22747	mycoplasma	522	4	8.2	19	1	LPRM_STAAR	P03063	staphylococ
450	5	10.2	1062	1	UL70_HCMVA	P17149	human cytom	523	4	8.2	25	1	GUN1_CLOJO	P78777	clostridium
451	5	10.2	1069	1	S24B_ARATH	Q9m081	arabidopsis	524	4	8.2	25	1	PRLA_ACHLY	P27459	achromobact
452	5	10.2	1076	1	NUPI_YEAST	P20676	saccharomyc	525	4	8.2	27	1	CXK7_CONPU	P56633	conus purpu
453	5	10.2	1086	1	NNTM_MOUSE	Q61941	mus musculu	526	4	8.2	36	1	NEUY_PIG	P01304	sus scrofa
454	5	10.2	1092	1	KPBB_HUMAN	Q93100	homo sapien	527	4	8.2	36	1	NEUY_RABIT	P09640	oryctolagus
455	5	10.2	1097	1	S24C_ARATH	Q9m291	arabidopsis	528	4	8.2	36	1	NEUY_RANRI	P29949	rana ridibu
456	5	10.2	1098	1	GRSA_BACBR	P14687	bacillus br	529	4	8.2	36	1	NEUY_SHEEP	P14765	ovis aries
457	5	10.2	1104	1	COLA_CLOPE	P43153	clostridium	530	4	8.2	37	1	CGRP_PIG	P30880	sus scrofa
458	5	10.2	1144	1	NOS2_MOUSE	P29477	mus musculu	531	4	8.2	37	1	CGRP_RANRI	P31888	rana ridibu
459	5	10.2	1146	1	CCAS_RAT	Q02485	rattus norv	532	4	8.2	37	1	GRP_SHEEP	P30881	ovis aries
460	5	10.2	1147	1	NOS2_RAT	Q06518	rattus norv	533	4	8.2	37	1	GRP_SHEEP	P24355	astasia lon
461	5	10.2	1147	1	NS2D_HUMAN	O60591	homo sapien	534	4	8.2	37	1	GRP_SHEEP	P24355	astasia lon
462	5	10.2	1169	1	Y785_RICPR	O05975	rickettsia	535	4	8.2	37	1	GRP_SHEEP	P48360	chlorella v
463	5	10.2	1187	1	PTNE_HUMAN	Q15678	homo sapien	536	4	8.2	37	1	GRP_SHEEP	P48360	chlorella v
464	5	10.2	1189	1	PTNE_MOUSE	Q82130	mus musculu	537	4	8.2	37	1	GRP_SHEEP	P48360	chlorella v
465	5	10.2	1189	1	PTNE_MOUSE	Q82130	mus musculu	538	4	8.2	37	1	GRP_SHEEP	P48360	chlorella v
466	5	10.2	1196	1	DNBI_HSV11	P78992	pichia past	539	4	8.2	37	1	GRP_SHEEP	P48360	chlorella v
467	5	10.2	1196	1	DNBI_HSV1F	P04296	herpes simp	540	4	8.2	37	1	GRP_SHEEP	P48360	chlorella v
468	5	10.2	1196	1	DNBI_HSV1F	P17469	herpes simp	541	4	8.2	37	1	GRP_SHEEP	P48360	chlorella v
469	5	10.2	1196	1	DNBI_HSV2H	P17470	herpes simp	542	4	8.2	37	1	GRP_SHEEP	P48360	chlorella v
470	5	10.2	1196	1	DNBI_HSV2H	P89452	herpes simp	543	4	8.2	37	1	GRP_SHEEP	P48360	chlorella v
471	5	10.2	1219	1	YH29_YEAST	P36384	herpes simp	544	4	8.2	37	1	GRP_SHEEP	P48360	chlorella v
						Q04439	saccharomyc								

545	4	8.2	37	1	RR36_SPIOL	P12230 spinacia ol	618	4	8.2	68	1	ATX1_RAT	Q9wuc4 rattus norv
546	4	8.2	37	1	RR36_TOBAC	P12144 nicotiana t	619	4	8.2	68	1	ATX1_SHEEP	Q0xt28 ovis aries
547	4	8.2	37	1	RL36_AQUAE	O66487 aquifex ae	620	4	8.2	69	1	YLAI_BACSU	O07633 bacillus su
548	4	8.2	37	1	RL36_BACST	P07841 bacillus st	621	4	8.2	70	1	PSAE_CYPAP	P48114 cyanophora
549	4	8.2	37	1	RL36_BORBU	O51452 borrelia bu	622	4	8.2	70	1	YAJM_RHLSN	P55513 rhizobium s
550	4	8.2	37	1	RL36_CAMJE	Q9pm84 campylobact	623	4	8.2	70	1	YIM6_BPPH1	P10430 bacterioph
551	4	8.2	37	1	RL36_DEIRA	Q9rsko deinococcus	624	4	8.2	71	1	ACAL_ACALU	P81592 acalolepta
552	4	8.2	37	1	RL36_HAEIN	P46361 haemophilus	625	4	8.2	72	1	SP23_HUMAN	P22532 homo sapien
553	4	8.2	37	1	RL36_HELPJ	Q9zjtl helicobacte	626	4	8.2	73	1	MT_DREPO	Q94550 dreisassa p
554	4	8.2	37	1	RL36_HELPJ	P56058 helicobacte	627	4	8.2	73	1	RK27_CHRAL	P41549 chrysoschro
555	4	8.2	37	1	RL36_LEPIN	O9xd13 leptospira	628	4	8.2	74	1	WDNM_RAT	P14730 rattus norv
556	4	8.2	37	1	RL36_MYCGE	P47420 mycoplasma	629	4	8.2	75	1	YCX1_PORPU	P51336 porphyra pu
557	4	8.2	37	1	RL36_MYCLE	Q9x7a2 mycobacteri	630	4	8.2	76	1	RS37_YEAST	P05759 saccharomyc
558	4	8.2	37	1	RL36_MYCPN	P52864 mycoplasma	631	4	8.2	77	1	YDCE_ECOLI	P31992 escherichia
559	4	8.2	37	1	RL36_MYGSP	P38015 mycoplasma	632	4	8.2	78	1	S10D_RAT	P02634 rattus norv
560	4	8.2	37	1	RL36_MYCTU	P45810 mycobacteri	633	4	8.2	78	1	YCX1_DICDH	P30160 dictyocha di
561	4	8.2	37	1	RL36_STRCO	O86772 streptomyce	634	4	8.2	78	1	YD80_METJA	Q58775 methanococc
562	4	8.2	37	1	RL36_SYNPE	O24707 synecococc	635	4	8.2	78	1	Y009_BPL2	P42544 bacterioph
563	4	8.2	37	1	RL36_THETH	P80256 thermus aqu	636	4	8.2	79	1	NSGX_HUMAN	Q9uh64 homo sapien
564	4	8.2	37	1	RL36_TREPA	O83239 treponema p	637	4	8.2	79	1	YIAO_BACSU	P37509 bacillus su
565	4	8.2	37	1	RL36_UREPA	Q9pqn7 ureaplasma	638	4	8.2	81	1	PORD_METH	P56815 methanobact
566	4	8.2	37	1	RL36_VIBCH	P78001 vibrio chol	639	4	8.2	82	1	RBS_SINAL	P13951 sinapis alb
567	4	8.2	37	1	SKK2_LEIQH	P45628 leiurus qui	640	4	8.2	82	1	Y056_NPVOP	O10314 orgyia pseu
568	4	8.2	38	1	RL36_BUCAI	P57570 buchera ap	641	4	8.2	82	1	YKD3_CAEEL	Q03561 caenorhabdi
569	4	8.2	38	1	RL36_ECOLI	P21194 escherichia	642	4	8.2	83	1	CNCG_BOVIN	P22571 bos taurus
570	4	8.2	38	1	RL36_LACIA	P27146 lactococcus	643	4	8.2	83	1	CNCG_HUMAN	Q13956 homo sapien
571	4	8.2	38	1	RL36_SYNY3	P73300 synecocyst	644	4	8.2	83	1	CNCG_SPETR	O55175 spermophilu
572	4	8.2	39	1	AMP1_CHICK	P80389 gallus gall	645	4	8.2	84	1	YBFJ_ECOLI	P46146 escherichia
573	4	8.2	39	1	GLL2_CHICK	P46157 gallus gall	646	4	8.2	84	1	YS14_CAEEL	Q09362 caenorhabdi
574	4	8.2	40	1	UPKB_MOUSE	Q922c6 mus musculu	647	4	8.2	86	1	NI2B_PEA	Q00665 pisum sativ
575	4	8.2	43	1	NT3_RAJCL	P25434 raja clavata	648	4	8.2	86	1	SELW_SHEEP	O19097 ovis aries
576	4	8.2	43	1	PSBN_CYPAP	P48108 cyanophora	649	4	8.2	86	1	YIDD_PROMI	P22834 proteus mir
577	4	8.2	44	1	FMF2_SCHPO	P45846 sus scrofa	650	4	8.2	87	1	CNRG_BOVIN	Q04972 bos taurus
578	4	8.2	44	1	PSBN_CHLRE	Q34069 schizosacch	651	4	8.2	87	1	CNRG_CANFA	P54827 canis fami
579	4	8.2	44	1	PSBN_CHLRE	Q06480 chlamydomon	652	4	8.2	87	1	CNRG_MOUSE	P18545 homo sapien
580	4	8.2	44	1	PSBN_NEPOL	Q9tkw6 nephroselmi	653	4	8.2	87	1	CNRG_MOUSE	P09174 mus musculu
581	4	8.2	45	1	RL36_CHLPN	Q9z6x0 chlamydia p	654	4	8.2	87	1	RR15_TOBAC	P06373 nicotiana t
582	4	8.2	45	1	RL36_CHLTR	O84791 chlamydia t	655	4	8.2	89	1	DYLL_HUMAN	Q9y3p0 homo sapien
583	4	8.2	45	1	RS22_ECOLI	P28690 escherichia	656	4	8.2	89	1	NEUY_MOUSE	P57774 mus musculu
584	4	8.2	46	1	AX1_BETVU	P81493 beta vulgar	657	4	8.2	89	1	RL34_METJA	P54053 methanococc
585	4	8.2	46	1	GCH1_BACPU	P48063 bacillus pu	658	4	8.2	89	1	SV18_HUMAN	P55774 h small ind
586	4	8.2	49	1	DISI_ECHCA	P17347 echis carin	659	4	8.2	90	1	DBH_BACST	P02346 bacillus st
587	4	8.2	49	1	Y3K8_SSVI	P20204 sulfolobus	660	4	8.2	90	1	DBH_THEMEA	P02346 thermotoga
588	4	8.2	49	1	YBHT_ECOLI	P75759 escherichia	661	4	8.2	90	1	HBA1_UROHA	P18979 uromastix h
589	4	8.2	50	1	ITH2_BOVIN	P56651 bos taurus	662	4	8.2	90	1	NOLS_RHIME	Q52975 rhizobium m
590	4	8.2	50	1	YACG_ECOLI	P36681 escherichia	663	4	8.2	90	1	RS15_CAMJE	P49392 campylobact
591	4	8.2	51	1	INS_ACOCA	P01324 acomyx cahi	664	4	8.2	91	1	ACCD_ANTFO	Q31796 anthoceros
592	4	8.2	51	1	INS_ANGRO	P42633 anguilla ro	665	4	8.2	91	1	Y909_METJA	Q58319 methanococc
593	4	8.2	51	1	INS_BALPH	P01312 balaenopter	666	4	8.2	92	1	ARN_BPT4	P39510 bacterioph
594	4	8.2	51	1	INS_DIDMA	P18109 didelphis m	667	4	8.2	92	1	CAL_CANFA	P41547 canis fami
595	4	8.2	52	1	INS_PIAME	P81881 piaractus m	668	4	8.2	92	1	DBH_BACSU	P08821 bacillus su
596	4	8.2	52	1	RUBR_MEGEL	P00271 megasphaera	669	4	8.2	92	1	IM13_DROME	Q9vtn3 drosophila
597	4	8.2	54	1	APR_HUMAN	Q13794 homo sapien	670	4	8.2	92	1	YLC1_YEREN	P16161 yersinia en
598	4	8.2	55	1	ATP8_ANAPL	P50655 anas platyr	671	4	8.2	93	1	E311_ADE05	P17590 human adeno
599	4	8.2	55	1	ATP8_LOXNO	Q9mdj1 loxigilla n	672	4	8.2	93	1	HMEN_SCHAM	P14150 schistocerc
600	4	8.2	55	1	ATP8_SQAC	Q9z250 squallus aca	673	4	8.2	93	1	IFHB_BUCAP	Q44654 buchnera ap
601	4	8.2	55	1	ATP8_XENIA	P03931 xenopus lae	674	4	8.2	93	1	NI2A_MEDSA	Q40361 medicago sa
602	4	8.2	55	1	ISH1_STOHE	P31713 stoichactis	675	4	8.2	93	1	Y073_METJA	Q60379 methanococc
603	4	8.2	56	1	ANCI_APIME	P56682 apis mellif	676	4	8.2	93	1	YF83_YEAST	O14464 saccharomyc
604	4	8.2	56	1	RL32_ECOLI	P02435 escherichia	677	4	8.2	93	1	YQIC_CAEEL	Q09283 caenorhabdi
605	4	8.2	59	1	PSBK_PINTH	P41598 pinus thunb	678	4	8.2	94	1	AFP_ASPGI	P17337 aspergillus
606	4	8.2	59	1	ATP8_BPP22	P57017 bacterioph	679	4	8.2	94	1	CKS1_CAEEL	Q17868 caenorhabdi
607	4	8.2	61	1	ATP8_CHEMY	Q9xpi2 chelonilla my	680	4	8.2	94	1	DBH_HELPJ	Q92108 helicobacte
608	4	8.2	61	1	IPST_ANGAN	P11705 anguilla an	681	4	8.2	94	1	DBH_HELPJ	O25506 helicobacte
609	4	8.2	61	1	NO14_PEA	P26415 pisum sativ	682	4	8.2	94	1	IFHB_ECOLI	P08756 escherichia
610	4	8.2	64	1	Y592_HAEIN	P44021 haemophilus	683	4	8.2	94	1	IFHB_ERWCH	P37983 erwina chr
611	4	8.2	65	1	GLL1_CHICK	P46156 gallus gall	684	4	8.2	94	1	IFHB_PSEAE	Q51473 pseudomonas
612	4	8.2	65	1	YCX2_GUITH	O78421 guillardia	685	4	8.2	94	1	IFHB_SERMA	P23303 serratia ma
613	4	8.2	66	1	SECE_RICPR	P50054 rickettsia	686	4	8.2	95	1	VP10_NPVAC	Q40870 autographa
614	4	8.2	67	1	ATPE_SCHPO	P87316 schizosacch	687	4	8.2	95	1	CH10_BORPE	P48221 bordetella
615	4	8.2	67	1	DISB_ECHCA	P81631 echis carin	688	4	8.2	95	1	DBH_THETH	P19436 thermus aqu
616	4	8.2	68	1	ATOX_HUMAN	O00244 homo sapien	689	4	8.2	95	1	RL31_UREPA	Q9prel ureaplasma
617	4	8.2	68	1	ATOX_MOUSE	O08997 mus musculu	690	4	8.2	95	1	U119_CANFA	Q19177 canis fami

691	4	8.2	96	1	RL4_XENTR	P14117 xenopus tro	764	4	8.2	110	1	INS2_MOUSE	P01326 mus musculus
692	4	8.2	97	1	BOR_LAMB	P26814 bacterioph	765	4	8.2	110	1	INS2_RAT	P01323 rattus norv
693	4	8.2	97	1	NEUY_CHICK	P28673 gallus gall	766	4	8.2	110	1	INS_CANFA	P01321 canis fami
694	4	8.2	97	1	NEUY_HUMAN	P01303 homo sapien	767	4	8.2	110	1	INS_CERAE	P30407 cercopithe
695	4	8.2	97	1	NEUY_XENIA	P33689 xenopus lae	768	4	8.2	110	1	INS_CRILO	P01313 cricetus
696	4	8.2	97	1	N075_MEDSA	P11728 medicago sa	769	4	8.2	110	1	INS_HUMAN	P01308 homo sapien
697	4	8.2	97	1	RL31_MICPN	P78020 mycoplasma	770	4	8.2	110	1	INS_MACFA	P30406 macaca fasc
698	4	8.2	97	1	NEUY_RAT	P07808 rattus norv	771	4	8.2	110	1	INS_PANFA	P30410 pan troglod
699	4	8.2	98	1	NEUY_TORMA	P28674 torpedo mar	772	4	8.2	110	1	INS_RABIT	P01311 oryctolagus
700	4	8.2	98	1	VE7_HPV58	P26557 human papil	773	4	8.2	110	1	INS_RABIT	P01311 oryctolagus
701	4	8.2	98	1	VG04_BPMD2	P64200 mycobacteri	774	4	8.2	110	1	LZ8_CANLU	P14945 ganoderma 1
702	4	8.2	98	1	YX17_BACSU	P43220 bacillus su	775	4	8.2	110	1	N12A_PSA	P20959 pisum sativ
703	4	8.2	99	1	CH10_MCAV	O86017 mycobacteri	776	4	8.2	110	1	YLCC_ECOLI	P77214 escherichia
704	4	8.2	99	1	CH10_MYCB	P15020 mycobacteri	777	4	8.2	111	1	FREA_HUMAN	P43638 homo sapien
705	4	8.2	99	1	CH10_MYCB	P24301 mycobacteri	778	4	8.2	111	1	FREA_MOUSE	O61574 mus musculus
706	4	8.2	99	1	CH10_MYCTU	P09621 mycobacteri	779	4	8.2	111	1	RLA3_LEINI	O6382 leishmania
707	4	8.2	99	1	RS20_CHLNU	O927f2 chlamydia p	780	4	8.2	111	1	YH07_YEAST	O6382 leishmania
708	4	8.2	100	1	IHF8_PSEPU	Q52285 pseudomonas	781	4	8.2	112	1	CISY_BARVB	P38804 saccharomyc
709	4	8.2	100	1	N012_VICSA	P44701 vicia sativ	782	4	8.2	112	1	FERY_CAUCR	P51035 bartonella
710	4	8.2	100	1	Y953_METJA	Q58363 methanococc	783	4	8.2	112	1	OLF8_MOUSE	O45972 caulobacter
711	4	8.2	101	1	TBCA_ARATH	O04350 arabidopsis	784	4	8.2	112	1	RLA3_TRYCR	O60892 mus musculus
712	4	8.2	102	1	MTBR_METWA	P80655 methanosarc	785	4	8.2	112	1	VNUN_BPHK0	P26795 trypanosoma
713	4	8.2	102	1	VE7_PAPVD	P03131 deer papill	786	4	8.2	112	1	Y122_CAEEL	P18683 bacterioph
714	4	8.2	102	1	Y266_BORBU	P11332 european el	787	4	8.2	112	1	YE14_YEAST	P03935 caenorhabdi
715	4	8.2	102	1	CYTL_PIG	Q44754 borrelia bu	788	4	8.2	112	1	YPMC_ECOLI	P39973 saccharomyc
716	4	8.2	103	1	LAC_CHICK	P20763 gallus gall	789	4	8.2	113	1	GTHB_MURCI	P07115 escherichia
717	4	8.2	103	1	N012_MEDPR	P30365 medicago tr	790	4	8.2	113	1	N12B_MEDSA	P12837 muraesox
718	4	8.2	103	1	Y4A0_MYCPN	P75074 mycoplasma	791	4	8.2	113	1	Y076_METJA	Q40339 methanoco
719	4	8.2	104	1	CMGA_STRCA	P33716 struthio ca	792	4	8.2	113	1	Y076_METJA	Q40339 methanoco
720	4	8.2	104	1	RN30_RANPI	P22069 rana pipien	793	4	8.2	114	1	ET3_RABIT	P19998 oryctolagus
721	4	8.2	104	1	YX17_BACSU	P04500 bacillus su	794	4	8.2	114	1	YEJG_ECOLI	P33917 escherichia
722	4	8.2	104	1	YX17_BACSU	P04500 bacillus su	795	4	8.2	114	1	YEJG_ECOLI	P33917 escherichia
723	4	8.2	105	1	YX17_BACSU	P04500 bacillus su	796	4	8.2	115	1	ALX1_PIG	P22298 sus scrofa
724	4	8.2	105	1	YX17_B								

837	4	8.2	121	1	HESB_PLEBO	P46053 plectonema	910	4	8.2	135	1	ANFC_SQUAC	P41319 squalus aca
838	4	8.2	121	1	MP70_MYCKA	Q49614 mycobacteri	911	4	8.2	135	1	CYB_APUPAP	Q33629 apus apus (
839	4	8.2	121	1	UBCC_ARATH	P56617 arabadopsis	912	4	8.2	135	1	EBSB_ENTFA	P36921 enterococcu
840	4	8.2	122	1	H2B_ARATH	P40283 arabadopsis	913	4	8.2	135	1	FKB2_YEAST	P32472 saccharomyc
841	4	8.2	122	1	Y22B_METJA	P81305 methanococc	914	4	8.2	135	1	FKB2_YEAST	P56793 arabadopsis
842	4	8.2	123	1	HEB1_ANAVA	P46051 anabena va	915	4	8.2	135	1	RR16_ARATH	P21512 euglena gra
843	4	8.2	123	1	HEB2_ANAVA	P46052 anabena va	916	4	8.2	135	1	RR16_EUGGR	P08526 homo sapien
844	4	8.2	123	1	Y052_NPVAC	P41456 autographa	917	4	8.2	135	1	RL27_HUMAN	Q29136 archaeoglob
845	4	8.2	123	1	YB44_YEAST	P38305 saccharomyc	918	4	8.2	135	1	RS9_ARCFU	Q10516 mycobacteri
846	4	8.2	123	1	Y002_CABEL	P34634 caenorhabdi	919	4	8.2	136	1	YM33_MYCTU	P70160 mus musculu
847	4	8.2	124	1	CB21_RAPSA	P14584 raphanus sa	920	4	8.2	136	1	CAL0_RAT	P01257 rattus norv
848	4	8.2	124	1	HV1D_HUMAN	P01760 homo sapien	921	4	8.2	136	1	CAL1_ONCKE	P01263 oncorhynch
849	4	8.2	124	1	HV1E_HUMAN	P01761 homo sapien	922	4	8.2	136	1	R27A_SCHPO	O14388 schizosacch
850	4	8.2	124	1	RL17_MYCPN	Q59547 mycoplasma	923	4	8.2	136	1	R27B_SCHPO	O14388 schizosacch
851	4	8.2	124	1	SPOF_BACSU	P06628 bacillus su	924	4	8.2	136	1	RL27_CAEEL	P01914 caenorhabdi
852	4	8.2	124	1	VG04_VACCV	P21025 vaccinia vi	925	4	8.2	137	1	5H4_PIG	Q29006 sus scrofa
853	4	8.2	124	1	VG04_VARY	P32994 variola vir	926	4	8.2	137	1	H2B4_MAIZE	P49120 zea mays (m
854	4	8.2	124	1	YLS1_CABEL	P34386 caenorhabdi	927	4	8.2	137	1	LSM4_MOUSE	Q9qxa5 mus musculu
855	4	8.2	125	1	CALR_CHICK	P10286 gallus gall	928	4	8.2	137	1	MP12_LYNST	P25289 lymanaea sta
856	4	8.2	125	1	HV1F_HUMAN	P06336 homo sapien	929	4	8.2	137	1	RR16_VIGUN	P42353 vigina ungu
857	4	8.2	125	1	RL7_LIBAF	P41189 liberobacte	930	4	8.2	137	1	RR9_CHLVU	P56358 chlorella v
858	4	8.2	125	1	RS17_CABEL	O01692 caenorhabdi	931	4	8.2	137	1	WAP_RAT	P01174 rattus norv
859	4	8.2	125	1	RS6_HAEIN	P44375 haemophilus	932	4	8.2	138	1	CAL_CHICK	P07660 gallus gall
860	4	8.2	125	1	Y394_RICPR	Q9zdd7 rickettsia	933	4	8.2	138	1	DSBH_BACSU	Q32217 bacillus su
861	4	8.2	126	1	CD59_RAT	P27274 rattus norv	934	4	8.2	138	1	GCSH_PYRAB	Q9v0g1 pyrococcus
862	4	8.2	126	1	NG24_MOUSE	Q9z1q4 mus musculu	935	4	8.2	138	1	GTH2_CLAGA	P53543 clarias gar
863	4	8.2	126	1	WNT1_EUMSK	P28113 eumeces ski	936	4	8.2	138	1	HEX9_ADE07	P30283 human adeno
864	4	8.2	126	1	WNT1_PITME	P28139 pituophis m	937	4	8.2	138	1	ID5A_ADEPA	P09941 adenanthera
865	4	8.2	126	1	WNT1_SCHPO	P28141 sceloporus	938	4	8.2	138	1	PT56_SACKL	Q02997 saccharomyc
866	4	8.2	126	1	YAME_SCHPO	Q10188 schizosacch	939	4	8.2	138	1	VIVA_BPT7	P03723 bacterioph
867	4	8.2	127	1	CAL2_HUMAN	P10092 homo sapien	940	4	8.2	138	1	X_HPEGS	Q03168 ground squi
868	4	8.2	127	1	HOL2_HOLDI	Q25054 holotrichia	941	4	8.2	138	1	Y178_RICPR	Q9zdv5 rickettsia
869	4	8.2	127	1	YF51_HELPY	O26075 helicobacte	942	4	8.2	139	1	LSM4_HUMAN	Q9y4z0 homo sapien
870	4	8.2	128	1	CAL1_HUMAN	P06881 homo sapien	943	4	8.2	139	1	NUSB_ECOLI	P04381 escherichia
871	4	8.2	128	1	CAL1_RAT	P01256 rattus norv	944	4	8.2	139	1	YRKR_BACSU	P34445 bacillus su
872	4	8.2	128	1	HSL0_SALTY	O30911 salmonella	945	4	8.2	140	1	CSF2_CAVPO	Q50481 cavia porce
873	4	8.2	128	1	IF5A_ARCFU	O29612 archaeoglob	946	4	8.2	140	1	GTH2_ANGAN	P27767 anguilla an
874	4	8.2	128	1	KV1X_HUMAN	P01637 mus musculu	947	4	8.2	140	1	YNU5_YEAST	P40162 saccharomyc
875	4	8.2	128	1	KV5E_MOUSE	P07615 vaccinia vi	948	4	8.2	140	1	YQIB_ECOLI	P36652 escherichia
876	4	8.2	128	1	VL05_VACCV	P33043 variola vir	949	4	8.2	140	1	Y006_METJA	O60305 methanococ
877	4	8.2	129	1	CARP_MOUSE	P56388 mus musculu	950	4	8.2	141	1	ARSC_YEREN	P74984 yersinia en
878	4	8.2	129	1	CARP_RAT	P49192 rattus norv	951	4	8.2	141	1	CAL0_HUMAN	P01258 homo sapien
879	4	8.2	129	1	KV1W_HUMAN	P04431 homo sapien	952	4	8.2	141	1	CSF2_MOUSE	P01587 mus musculu
880	4	8.2	129	1	KV1X_HUMAN	P04432 homo sapien	953	4	8.2	141	1	VTU1_DROME	P11449 drosophila
881	4	8.2	129	1	RL7_TREPA	O83268 treponema p	954	4	8.2	141	1	YK13_YEAST	P36128 saccharomyc
882	4	8.2	129	1	RL7_CHICK	P08636 gallus gall	955	4	8.2	142	1	AP17_HUMAN	P53680 homo sapien
883	4	8.2	129	1	VMOR_BPMU	P23848 bacterioph	956	4	8.2	142	1	AP17_MOUSE	Q00380 mus musculu
884	4	8.2	129	1	YEQ2_YEAST	P40046 saccharomyc	957	4	8.2	142	1	RHIC_ORYRH	O76145 oryctes rhl
885	4	8.2	129	1	YP73_GVCL	P41730 cryptophleb	958	4	8.2	142	1	RR40_SPIOL	P27684 spinacia ol
886	4	8.2	130	1	CV36_YEAST	P25603 saccharomyc	959	4	8.2	142	1	RL16_THEMA	P38509 thermotoga
887	4	8.2	130	1	MIA_MOUSE	O61865 mus musculu	960	4	8.2	142	1	RS6_HELPY	Q9zjvl helicobacte
888	4	8.2	130	1	MIA_RAT	O62946 rattus norv	961	4	8.2	142	1	RS6_HELPY	P56013 helicobacte
889	4	8.2	130	1	Y060_BPT4	P39222 bacterioph	962	4	8.2	142	1	VG09_BPT4	P40820 bacterioph
890	4	8.2	130	1	YEW5_YEAST	P40082 saccharomyc	963	4	8.2	142	1	YIC9_YEAST	P40538 saccharomyc
891	4	8.2	130	1	YHFU_ECOLI	P45547 escherichia	964	4	8.2	143	1	CAL_SHEEP	P01261 ovis aries
892	4	8.2	130	1	YKL5_YEAST	P36073 saccharomyc	965	4	8.2	143	1	GCS1_AQUAE	O67151 aquifex aeo
893	4	8.2	131	1	CAIF_ECOLI	O47081 escherichia	966	4	8.2	143	1	HMGB_TETH	P40626 tetrahymena
894	4	8.2	131	1	CHHB_BOMMO	P05688 bombyx mori	967	4	8.2	143	1	RL16_MARPO	P06383 marchantia
895	4	8.2	131	1	HSLR_HAEIN	P44754 haemophilus	968	4	8.2	144	1	BT12_BLOTA	Q17282 blomia trop
896	4	8.2	131	1	MIA_HUMAN	Q16674 homo sapien	969	4	8.2	144	1	END2_BPT4	P07059 bacterioph
897	4	8.2	132	1	ALK1_HUMAN	P03973 homo sapien	970	4	8.2	144	1	IL9_MOUSE	P15247 mus musculu
898	4	8.2	132	1	HSLR_AERSA	Q42464 aethemonas s	971	4	8.2	144	1	RL16_BACHD	Q9z9k7 bacillus ha
899	4	8.2	132	1	IF5A_METJA	O58625 methanococc	972	4	8.2	144	1	RL16_BACSU	P14577 bacillus su
900	4	8.2	132	1	RRF_CLOPE	Q46293 clostridium	973	4	8.2	145	1	AZUP_PARDT	P80401 paracoccus
901	4	8.2	132	1	RS8_RICPR	Q9zcr9 rickettsia	974	4	8.2	145	1	CYTF_HUMAN	O76096 homo sapien
902	4	8.2	133	1	AGSW_BOVIN	Q29414 bos taurus	975	4	8.2	145	1	H2B_CAPAN	O49118 capsicum an
903	4	8.2	133	1	CYB5_HUMAN	P00167 homo sapien	976	4	8.2	145	1	PA21_BOVIN	P00593 bos taurus
904	4	8.2	133	1	PA23_OXYSC	P00616 oxyuranus s	977	4	8.2	145	1	PK18_PEA	P11891 pisum sativ
905	4	8.2	133	1	PA2D_PSETE	P23028 pseudonaja	978	4	8.2	145	1	YGL3_SYNY3	P73841 synechocyst
906	4	8.2	134	1	CAL2_RAT	P10093 rattus norv	979	4	8.2	145	1	YPH2_MYCCA	P45614 mycoplasma
907	4	8.2	134	1	RS17_CRIGR	P06584 cricetus	980	4	8.2	146	1	H2B_TOBAC	P93354 nicotiana t
908	4	8.2	134	1	RS17_HUMAN	P08708 homo sapien	981	4	8.2	147	1	AP17_YEAST	Q00381 saccharomyc
909	4	8.2	134	1	RS17_RAT	P04644 rattus norv	982	4	8.2	147	1	H2B_GOSHI	O22582 gossypium h



FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 297 AA; 32745 MW; FC72A7F3A8EBF67C CRC64;

Query Match 98.0%; Score 48; DB 1; Length 297;  
Best Local Similarity 100.0%; Pred. No. 4.3e-44;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNNDFEVEFVPCISCSNNPTCWAICKRIPNKKPGK 48  
|||||  
DB 149 KORQKPPSKPNNDFEVEFVPCISCSNNPTCWAICKRIPNKKPGK 196

RESULT 3

VGLG\_HRSV3  
ID VGLG\_HRSV3 STANDARD; PRT; 297 AA.  
AC P27022;

DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
GN G.

OS Human respiratory syncytial virus (strain rsb1734).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

CC Paramyxoviridae; Pneumovirinae; Pneumovirus.

OX NCBI\_TaxID=11253;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91374005; PubMed=1895054;

RA Cane P.A., Matthews D.A., Pringle C.R.;

RT "Identification of variable domains of the attachment (G) protein of

subgroup A respiratory syncytial viruses.";

RL J. Gen. Virol. 72:2091-2096(1991).

CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE

RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND

HEMAGGLUTININATING ACTIVITIES.

CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED

CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS

DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

DR PIR: JQ1205; JQ1205.

DR InterPro: IPR000925; -.

DR Pfam: PF00802; Glycoprotein\_G; 1.

KW Transmembrane; Glycoprotein.

FT DOMAIN 1 37

FT TRANSMEM 38 66

FT DOMAIN 67 297

FT CARBOHYD 135 135

FT CARBOHYD 237 237

FT CARBOHYD 251 251

SQ SEQUENCE 297 AA; 32525 MW; 48448F9E091E1802 CRC64;

Query Match

Best Local Similarity 98.0%; Score 48; DB 1; Length 297;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNNDFEVEFVPCISCSNNPTCWAICKRIPNKKPGK 48  
|||||  
DB 149 KORQKPPSKPNNDFEVEFVPCISCSNNPTCWAICKRIPNKKPGK 196

RESULT 4

VGLG\_HRSV4

ID VGLG\_HRSV4 STANDARD; PRT; 297 AA.

AC P27023;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-AUG-1992 (Rel. 23, Last annotation update)

DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).

GN G.

OS Human respiratory syncytial virus (strain rsb5857).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11254;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91374005; PubMed=1895054;

RA Cane P.A., Matthews D.A., Pringle C.R.;

RT "Identification of variable domains of the attachment (G) protein of

subgroup A respiratory syncytial viruses.";

RL J. Gen. Virol. 72:2091-2096(1991).

CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE

RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND

HEMAGGLUTININATING ACTIVITIES.

CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED

CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS

DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

DR PIR: JQ1206; JQ1206.

DR InterPro: IPR000925; -.

DR Pfam: PF00802; Glycoprotein\_G; 1.

KW Transmembrane; Glycoprotein.

FT DOMAIN 1 37

FT TRANSMEM 38 66

FT DOMAIN 67 297

FT CARBOHYD 85 85

FT CARBOHYD 103 103

FT CARBOHYD 135 135

FT CARBOHYD 237 237

FT CARBOHYD 251 251

FT CARBOHYD 294 294

SQ SEQUENCE 297 AA; 32772 MW; 10488CCA475936BE CRC64;

Query Match

Best Local Similarity 81.6%; Score 40; DB 1; Length 297;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDHFEEVFNPCISCSNNPTCWAICKRIPNKKPGK 49  
|||||

DB 158 KPNDHFEEVFNPCISCSNNPTCWAICKRIPNKKPGK 197

RESULT 5

VGLG\_HRSV6

ID VGLG\_HRSV6 STANDARD; PRT; 297 AA.

AC P27025;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-AUG-1992 (Rel. 23, Last annotation update)

DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).

GN G.

OS Human respiratory syncytial virus (strain rsb6256).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

CC Paramyxoviridae; Pneumovirinae; Pneumovirus.

OX NCBI\_TaxID=11256;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91374005; PubMed=1895054;

RA Cane P.A., Matthews D.A., Pringle C.R.;

RT "Identification of variable domains of the attachment (G) protein of

subgroup A respiratory syncytial viruses.";

RL J. Gen. Virol. 72:2091-2096(1991).

CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE

RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND

HEMAGGLUTININATING ACTIVITIES.

CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED

CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS

DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

DR PIR: JQ1208; JQ1208.

DR InterPro: IPR000925; -.

DR Pfam: PF00802; Glycoprotein\_G; 1.

KW Transmembrane; Glycoprotein.

FT DOMAIN 1 37

FT CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 38 66 POTENTIAL.  
FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 297 AA; 32708 MW; 6781756C38B64A80 CRC64;

Query Match 81.6%; Score 40; DB 1; Length 297;  
Best Local Similarity 100.0%; Pred. No. 1.4e-35;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 KPNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPKKK 49  
|||||  
DB 158 KPNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPKKK 197  
|||||

RESULT 6  
VGLG\_HRSVL  
ID VGLG\_HRSVL STANDARD; PRT; 298 AA.  
AC P20895;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
GN G.  
OS Human respiratory syncytial virus (subgroup A / strain Long).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11260;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87289657; PubMed=24411388;  
RA Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;  
RT "The G glycoprotein of human respiratory syncytial viruses of  
RT subgroups A and B: extensive sequence divergence between  
RT antigenically related proteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).  
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
CC HEMAGGLUTININATING ACTIVITIES.  
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS  
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M1212; AAA47411.1; .  
DR PIR; A32703; MGNZRL.  
DR InterPro; IPR000925; .  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
KW Transmembrane; Glycoprotein.  
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 38 66 POTENTIAL.  
FT DOMAIN 67 298 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 298 AA; 32781 MW; B79FEFA4B4A73B0E CRC64;

Query Match 81.6%; Score 40; DB 1; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.4e-35;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 KPNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPKKK 49  
|||||  
DB 158 KPNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPKKK 197  
|||||

RESULT 7  
VGLG\_HRSV7  
ID VGLG\_HRSV7 STANDARD; PRT; 297 AA.  
AC P27026;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
GN G.  
OS Human respiratory syncytial virus (strain rsb6614).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11257;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91374005; PubMed=1895054;  
RA Cane P.A., Matthews D.A., Pringle C.R.;  
RT "Identification of variable domains of the attachment (G) protein of  
RT subgroup A respiratory syncytial viruses.";  
RL J. Gen. Virol. 72:2091-2096(1991).  
CC -!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
CC HEMAGGLUTININATING ACTIVITIES.  
CC -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
CC -!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS  
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.  
CC PIR; JQ1209; JQ1209.  
DR InterPro; IPR000925; .  
DR Pfam; PF00802; Glycoprotein\_G; 1.  
KW Transmembrane; Glycoprotein.  
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 38 66 POTENTIAL.  
FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 297 AA; 32670 MW; 58B384028E437ACD CRC64;

Query Match 71.4%; Score 35; DB 1; Length 297;  
Best Local Similarity 100.0%; Pred. No. 2.9e-30;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 FHFEVFNPCSCSNNPTCWAICKRIPNKKPKKK 49  
|||||  
DB 163 FHFEVFNPCSCSNNPTCWAICKRIPNKKPKKK 197  
|||||

RESULT 8  
VGLG\_HRSV5  
ID VGLG\_HRSV5 STANDARD; PRT; 298 AA.  
AC P27024;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
GN G.  
OS Human respiratory syncytial virus (strain rsb6190).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11255;



```
DR InterPro: IPR000925; -.
DR Pfam: PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 292 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 292 AA; 32143 MW; 8EC60C85EF057BB5 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 292;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HFEVFNFPVCSIC 28
DB 164 HFEVFNFPVCSIC 176

RESULT 11
POLS_EEVP
ID POLS_EEVP STANDARD; PRT; 1255 AA.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE STRUCTURAL POLYPEPTIDE [CONTAINS: COAT PROTEIN C (EC 3.4.21.-); SPIKE
DE GLYCOPROTEINS E3, E2 AND E1; 6 KDA PEPTIDE].
OS Venezuelan equine encephalitis virus (strain p676).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=36385;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93079859; PubMed=1448915;
RA Kinney R.M., Tsuchiya K.R., Snider J.M., Trent D.W.;
RT "Genetic evidence that epizootic Venezuelan equine encephalitis (VEE)
RT viruses may have evolved from enzootic VEE subtype I-D virus.";
RL Virology 191:569-580(1992).
CC -!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
CC -!- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -!- MISCELLANEOUS: THE 6 KDA POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL
CC | SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
CC | HEMAGGLUTININ.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
CC -----
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CC -----
DR EMBL; L04653; AAC19319.1; -.
DR PIR; B44213; B44213.
DR HSSP; P03315; 1VCO.
DR MEROPS; S03.001.
DR InterPro; IPR000930; -.
DR InterPro; IPR000936; -.
DR InterPro; IPR001836; -.
DR InterPro; IPR002533; -.
DR InterPro; IPR002548; -.
DR Pfam; PF01589; Alpha_E1_glycop; 1.
DR Pfam; PF00943; Alpha_E2_glycop; 1.
DR Pfam; PF01563; Alpha_E3_glycop; 1.
DR Pfam; PF00944; Alpha_core; 1.
DR PRINTS; PR00798; TOGAVIRIN.
KW Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
KW serine protease.
FT CHAIN 1 275 COAT PROTEIN C (CAPSID PROTEIN C).
```

```
FT CHAIN 276 334 SPIKE GLYCOPROTEIN E3.
FT CHAIN 335 757 SPIKE GLYCOPROTEIN E2.
FT CHAIN 758 813 6 KDA PEPTIDE.
FT CHAIN 814 1255 SPIKE GLYCOPROTEIN E1.
FT ACT_SITE 152 152 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 158 158 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 226 226 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT TRANSMEM 702 722 POTENTIAL.
FT TRANSMEM 795 814 POTENTIAL.
FT TRANSMEM 1232 1249 POTENTIAL.
FT CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 652 652 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 947 947 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1255 AA; 138213 MW; 33CD302F5CAE8646 CRC64;

Query Match 14.3%; Score 7; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 PNKPKGK 48
DB 108 PNKPKGK 114

RESULT 12
RS13_STRCO
ID RS13_STRCO STANDARD; PRT; 126 AA.
AC 086773;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S13.
GN RPSM OR SC6G4.05.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D., Harris D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE BINDING OF FMET-TRNA AND, HENCE, IN THE
CC | INITIATION OF TRANSLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL; AL031317; CAA20383.1; -.
DR InterPro; IPR001892; -.
DR Pfam; PF00416; Ribosomal_S13; 1.
DR PROSITE; PS00646; RIBOSOMAL_S13; 1.
KW Ribosomal protein.
SQ SEQUENCE 126 AA; 14219 MW; F1E92BB01DE4906F CRC64;

Query Match 12.28%; Score 6; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 KPGKK 49
DB 121 KPGKK 126
```

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RESULT 13
ID Y021_CAEEEL STANDARD; PRT; 159 AA.
AC P34671;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE HYPOTHETICAL 18.0 KDA PROTEIN ZK688.1 IN CHROMOSOME III.
GN ZK688.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
FT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
FT elegans.";
RL Nature 368:32-38(1994).
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CC -----
CC EMBL; AF008591; AAC51657.1; -.
CC HSP; P15154; 1MH1.
CC MIM: 602050;
CC InterPro; IPR001806; -.
CC InterPro; IPR002380; -.
CC Pfam; PF00071; ras; 1.
CC PRINTS; PR00449; RASTRNSFRMG.
CC GTP-binding; Prenylation; Lipoprotein.
CC NP_BIND 10 17 GTP (BY SIMILARITY).
CC NP_BIND 57 61 GTP (BY SIMILARITY).
CC NP_BIND 115 118 GTP (BY SIMILARITY).
CC DOMAIN 32 40 EFFECTOR REGION (POTENTIAL).
CC LIPID 189 189 GERANYL-GERANYL (BY SIMILARITY).
CC SEQUENCE 192 AA; 21379 MW; 560BBC26BB7CDF4A CRC64;

Query Match 12.2%; Score 6; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 KPGKK 49
DB 183 KPGKK 188
|||||

RESULT 15
Y010_MYCPN STANDARD; PRT; 212 AA.
AC P75099;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN MG010 HOMOLOG (D12_ORF212).
GN MPN014 OR MPI40.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: SOME, TO DNA PRIMASES (DNAG).
CC -----
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CC -----
CC EMBL; L16621; AAA28226.1; -.
CC PIR; S44915; S44915.
CC WormPep; ZK688.1; CE00459.
CC Hypothetical protein.
CC SEQUENCE 159 AA; 18018 MW; 74280FC07F7FF633 CRC64;

Query Match 12.2%; Score 6; DB 1; Length 159;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PSKPN 13
DB 44 PSKPN 49
|||||

RESULT 14
RAC3_HUMAN STANDARD; PRT; 192 AA.
AC O14658;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 3 (P21-RAC3).
GN RAC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97400509; PubMed=9252344;
RA Haataja L., Groffen J., Heisterkamp N.;
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CC -----

DR EMBL: AF000016; AAB95788.1; -  
DR InterPro: IPR002936; -  
DR Pfam: PF01751; Toprim: 1.  
KW Hypothetical protein.  
SQ SEQUENCE 212 AA; 24497 MW; 24F971B162DEC2C3 CRC64;

Query Match 12.2%; Score 6; DB 1; Length 212;  
Best local Similarity 100.0%; Pred. No. 15;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NKPPSK 10  
      |||||  
Db 85 NKPPSK 90

Search completed: May 21, 2001, 14:19:40  
Job time: 103 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:17:52 ; Search time 19.59 Seconds  
(without alignments)  
293.169 Million cell updates/sec

Title: US-09-202-035-1  
Perfect score: 49  
Sequence: 1 KORONKPPSKPNDFHFEV.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Word size : 0

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL\_15:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49	100.0	233	14	Q9YVB3 human respi
2	48	98.0	292	14	Q9YVB2 human respi
3	48	98.0	295	14	Q86356 respiratory
4	48	98.0	295	14	Q86360 respiratory
5	48	98.0	297	14	Q82066 human respi
6	48	98.0	297	14	Q82067 human respi
7	48	98.0	297	14	Q82071 human respi
8	48	98.0	297	14	Q9YVB5 human respi
9	42	85.7	297	14	Q91947 human respi
10	41	83.7	297	14	Q82070 human respi
11	40	81.6	278	14	Q9Q6U1 human respi
12	40	81.6	278	14	Q9Q6T7 human respi
13	40	81.6	278	14	Q9Q6T4 human respi
14	40	81.6	278	14	Q9Q6T3 human respi
15	40	81.6	278	14	Q9Q6T1 human respi
16	40	81.6	278	14	Q9Q6T0 human respi
17	40	81.6	279	14	Q9Q6U0 human respi
18	40	81.6	279	14	Q9Q6T9 human respi
19	40	81.6	279	14	Q9Q6T8 human respi

Q9Q6T5 human respi

Q9Q6T2 human respi

Q9Q6S9 human respi

Q9Q6S7 human respi

Q9Q6S6 human respi

Q9Q6S3 human respi

Q9Q6S2 human respi

Q9Q6S1 human respi

Q9Q6S0 human respi

Q9Q6R9 human respi

Q9YVB0 human respi

Q86357 respiratory

Q86359 respiratory

Q82057 human respi

Q82058 human respi

Q82064 human respi

Q82072 human respi

Q82074 human respi

Q82078 human respi

Q82079 human respi

Q91944 human respi

Q91946 human respi

Q9YVC8 human respi

Q82065 human respi

Q82068 human respi

Q82073 human respi

Q82074 human respi

Q09634 human respi

Q09719 respiratory

Q01929 human respi

Q9Q6S4 human respi

Q86361 respiratory

Q82077 human respi

Q9Q6U2 human respi

Q9Q6T6 human respi

Q9Q6S8 human respi

Q9YVB1 human respi

Q86358 respiratory

Q82056 human respi

Q82060 human respi

Q82061 human respi

Q82062 human respi

Q82069 human respi

Q82075 human respi

Q82076 human respi

Q11978 human respi

Q9YVB4 human respi

Q91945 human respi

Q91UC4 human respi

Q9Q6S5 human respi

Q91UD7 human respi

Q91UE6 human respi

Q9Q6R8 human respi

Q9Q6R7 human respi

Q9Q6R6 human respi

Q9Q6R5 human respi

Q9Q6R4 human respi

Q9Q6R3 human respi

Q9Q6R2 human respi

Q9Q6R1 human respi

Q9Q6R0 human respi

Q9Q6Q9 human respi

Q9Q6Q8 human respi

Q91942 human respi

Q91943 human respi

Q9YVC9 human respi

Q36633 human respi

Q91941 human respi

Q91UD3 human respi

Q91UE1 human respi

Q91UC1 human respi

Q91UC7 human respi

Q91UD8 human respi

93	7	14.3	834	5	Q9V320	Q9V320 drosophila	166	6	12.2	1889	5	Q9XZS2	Q9XZS2 drosophila
94	7	14.3	1254	14	Q9YK4	Q9YK4 venezuelan	167	6	12.2	1889	5	Q9XZS1	Q9XZS1 drosophila
95	7	14.3	1468	10	Q9SVE1	Q9SVE1 arabidopsis	168	6	12.2	1889	5	Q9XZU9	Q9XZU9 drosophila
96	6	12.2	38	8	Q9MU8	Q9MU8 mesostigma	169	5	10.2	21	10	Q41181	Q41181 nicotiana t
97	6	12.2	77	6	Q02672	Q02672 aices alces	170	5	10.2	25	2	Q9R5G8	Q9R5G8 fusobacteri
98	6	12.2	94	5	Q9XUF3	Q9XUF3 caenorhabdi	171	5	10.2	40	4	Q16128	Q16128 homo sapien
99	6	12.2	109	14	Q9IUOC8	Q9IUOC8 human respi	172	5	10.2	49	2	Q9JVE5	Q9JVE5 neisseria m
100	6	12.2	111	4	Q9NQ12	Q9NQ12 homo sapien	173	5	10.2	61	2	Q05078	Q05078 borrelia bu
101	6	12.2	190	2	Q53760	Q53760 staphylococ	174	5	10.2	65	2	P73358	P73358 synechocyst
102	6	12.2	191	13	Q91874	Q91874 xenopus lae	175	5	10.2	65	10	Q9MGQ5	Q9MGQ5 medicago tr
103	6	12.2	192	13	Q93466	Q93466 gallus gall	176	5	10.2	70	4	Q9P1N2	Q9P1N2 homo sapien
104	6	12.2	196	10	Q40386	Q40386 nicotiana a	177	5	10.2	70	8	Q9ZYE1	Q9ZYE1 hippotragus
105	6	12.2	196	10	Q24103	Q24103 nicotiana a	178	5	10.2	70	8	Q9ZYE0	Q9ZYE0 hippotragus
106	6	12.2	205	5	Q18977	Q18977 caenorhabdi	179	5	10.2	70	8	Q9ZXD9	Q9ZXD9 hippotragus
107	6	12.2	206	1	Q59116	Q59116 pyrococcus	180	5	10.2	70	8	Q9ZXS1	Q9ZXS1 hippotragus
108	6	12.2	218	10	Q40381	Q40381 nicotiana a	181	5	10.2	70	8	Q9ZXR9	Q9ZXR9 hippotragus
109	6	12.2	243	10	Q9SYN7	Q9SYN7 arabidopsis	182	5	10.2	70	8	Q9ZXR8	Q9ZXR8 hippotragus
110	6	12.2	244	14	Q67697	Q67697 garlic viru	183	5	10.2	70	8	Q9ZXR7	Q9ZXR7 hippotragus
111	6	12.2	299	2	Q87489	Q87489 pseudomonas	184	5	10.2	70	8	Q9ZXR6	Q9ZXR6 hippotragus
112	6	12.2	317	5	Q44889	Q44889 caenorhabdi	185	5	10.2	70	8	Q9ZXR5	Q9ZXR5 hippotragus
113	6	12.2	359	10	Q23655	Q23655 arabidopsis	186	5	10.2	70	8	Q9ZXR4	Q9ZXR4 hippotragus
114	6	12.2	363	3	Q99326	Q99326 saccharomyc	187	5	10.2	76	8	Q34361	Q34361 damalisus
115	6	12.2	411	10	Q9SSG7	Q9SSG7 arabidopsis	188	5	10.2	78	9	Q37833	Q37833 bacterioph
116	6	12.2	415	10	Q9SFI6	Q9SFI6 arabidopsis	189	5	10.2	83	3	Q9U027	Q9U027 schistosacch
117	6	12.2	416	10	Q9SLK0	Q9SLK0 arabidopsis	190	5	10.2	84	2	Q9JXY3	Q9JXY3 neisseria m
118	6	12.2	418	2	Q54651	Q54651 streptococc	191	5	10.2	87	10	Q42237	Q42237 arabidopsis
119	6	12.2	418	3	Q9Y7V6	Q9Y7V6 emericella	192	5	10.2	90	9	Q9T1J5	Q9T1J5 bacterioph
120	6	12.2	454	2	Q53759	Q53759 staphylococ	193	5	10.2	90	14	Q9IGQ7	Q9IGQ7 tt virus. o
121	6	12.2	472	2	Q53779	Q53779 staphylococ	194	5	10.2	95	5	Q9U7I2	Q9U7I2 plasmodium
122	6	12.2	492	2	Q56193	Q56193 staphylococ	195	5	10.2	95	5	Q9U7I1	Q9U7I1 plasmodium
123	6	12.2	493	3	Q9UVD1	Q9UVD1 pneumocysti	196	5	10.2	95	5	Q9U7I0	Q9U7I0 plasmodium
124	6	12.2	515	5	Q76875	Q76875 drosophila	197	5	10.2	95	6	Q9U707	Q9U707 monodelphis
125	6	12.2	524	2	Q9LCB5	Q9LCB5 bacillus su	198	5	10.2	100	5	Q9V6C6	Q9V6C6 drosophila
126	6	12.2	544	1	P95960	P95960 sulfolobus	199	5	10.2	101	2	Q9ZLR3	Q9ZLR3 helicobacte
127	6	12.2	573	2	Q56192	Q56192 staphylococ	200	5	10.2	101	2	Q9RQNL	Q9RQNL vibrio chol
128	6	12.2	614	5	Q18636	Q18636 caenorhabdi	201	5	10.2	102	8	Q35106	Q35106 malaclemys
129	6	12.2	615	2	P94349	P94349 bacillus st	202	5	10.2	102	10	Q9SYR4	Q9SYR4 urtica dioi
130	6	12.2	631	5	Q9W556	Q9W556 drosophila	203	5	10.2	102	10	Q9S7L1	Q9S7L1 urtica dioi
131	6	12.2	641	2	Q9ZJA2	Q9ZJA2 helicobacte	204	5	10.2	102	10	Q9S7K8	Q9S7K8 urtica dioi
132	6	12.2	665	14	Q67649	Q67649 gibbon ape	205	5	10.2	103	1	Q9YFF7	Q9YFF7 aeropyrum p
133	6	12.2	666	2	Q53833	Q53833 staphylococ	206	5	10.2	104	5	Q15590	Q15590 entamoeba h
134	6	12.2	740	5	Q20760	Q20760 caenorhabdi	207	5	10.2	104	14	Q65267	Q65267 african swi
135	6	12.2	747	2	Q53832	Q53832 staphylococ	208	5	10.2	108	4	Q9UDD0	Q9UDD0 homo sapien
136	6	12.2	853	5	Q9U019	Q9U019 plasmodium	209	5	10.2	111	8	Q9MTN3	Q9MTN3 oenothera h
137	6	12.2	1023	3	Q9UOV6	Q9UOV6 yarrowia li	210	5	10.2	116	13	Q9YGP3	Q9YGP3 ictalurus p
138	6	12.2	1029	10	Q9SCT9	Q9SCT9 arabidopsis	211	5	10.2	119	1	Q9UX34	Q9UX34 sulfolobus
139	6	12.2	1199	5	Q76570	Q76570 caenorhabdi	212	5	10.2	120	2	Q52127	Q52127 lactobacill
140	6	12.2	1232	10	Q9SN91	Q9SN91 arabidopsis	213	5	10.2	120	4	Q60519	Q60519 homo sapien
141	6	12.2	1249	3	Q00647	Q00647 emericella	214	5	10.2	121	2	Q48877	Q48877 leptospira
142	6	12.2	1254	14	Q41516	Q41516 venezuelan	215	5	10.2	121	14	Q96671	Q96671 chicken ane
143	6	12.2	1254	14	Q9YKC9	Q9YKC9 venezuelan	216	5	10.2	121	14	Q39313	Q39313 chicken ane
144	6	12.2	1254	14	Q9YKC8	Q9YKC8 venezuelan	217	5	10.2	121	14	Q41448	Q41448 chicken ane
145	6	12.2	1254	14	Q9YKC7	Q9YKC7 venezuelan	218	5	10.2	121	14	Q9WB33	Q9WB33 chicken ane
146	6	12.2	1254	14	Q9WC26	Q9WC26 venezuelan	219	5	10.2	121	14	Q9J1K0	Q9J1K0 chicken ane
147	6	12.2	1255	14	Q66595	Q66595 venezuelan	220	5	10.2	121	14	Q9IZU6	Q9IZU6 chicken ane
148	6	12.2	1255	14	Q66593	Q66593 venezuelan	221	5	10.2	121	14	Q9IEZ4	Q9IEZ4 chicken ane
149	6	12.2	1255	14	Q90164	Q90164 venezuelan	222	5	10.2	122	14	Q9J5E5	Q9J5E5 fowlpox vir
150	6	12.2	1255	14	Q91628	Q91628 venezuelan	223	5	10.2	123	5	Q27070	Q27070 terebratul
151	6	12.2	1255	14	Q36300	Q36300 venezuelan	224	5	10.2	123	11	Q62379	Q62379 mus musculu
152	6	12.2	1255	14	Q36288	Q36288 venezuelan	225	5	10.2	124	2	Q48880	Q48880 leptospira
153	6	12.2	1255	14	Q98773	Q98773 venezuelan	226	5	10.2	124	2	Q9RV89	Q9RV89 deinococcus
154	6	12.2	1255	14	Q98775	Q98775 venezuelan	227	5	10.2	124	5	Q9W1C9	Q9W1C9 drosophila
155	6	12.2	1255	14	Q9WR91	Q9WR91 venezuelan	228	5	10.2	125	3	Q9P8P9	Q9P8P9 candida alb
156	6	12.2	1255	14	Q9WCF8	Q9WCF8 venezuelan	229	5	10.2	125	6	Q9N101	Q9N101 ovis aries
157	6	12.2	1255	14	Q9WCF7	Q9WCF7 venezuelan	230	5	10.2	126	10	Q9XHV7	Q9XHV7 oryza sativ
158	6	12.2	1255	14	Q9WCF6	Q9WCF6 venezuelan	231	5	10.2	127	8	Q99275	Q99275 centropomus
159	6	12.2	1255	14	Q9WCF4	Q9WCF4 venezuelan	232	5	10.2	127	8	Q9TG62	Q9TG62 centropomus
160	6	12.2	1255	14	Q36287	Q36287 venezuelan	233	5	10.2	130	8	Q9T9P3	Q9T9P3 gerris baba
161	6	12.2	1261	2	P73926	P73926 synechocyst	234	5	10.2	130	8	Q9T9F0	Q9T9F0 gerris yezo
162	6	12.2	1277	13	Q98902	Q98902 fugu rubrip	235	5	10.2	130	8	Q9T9E9	Q9T9E9 gerris yezo
163	6	12.2	1651	5	Q45176	Q45176 caenorhabdi	236	5	10.2	130	8	Q9T9E4	Q9T9E4 limnoporus
164	6	12.2	1811	5	Q9XZU8	Q9XZU8 drosophila	237	5	10.2	130	8	Q9T9E2	Q9T9E2 neogerris p
165	6	12.2	1887	5	Q9VYX6	Q9VYX6 drosophila	238	5	10.2	130	8	Q9T9E0	Q9T9E0 limnogonus

239	5	10.2	130	8	Q9T4Q3	Q9T4Q3	gerris grac	312	5	10.2	175	14	Q9PZS5	Q9PZS5	human cytom
240	5	10.2	131	8	Q9T9F2	Q9T9F2	gerris nepa	313	5	10.2	175	14	Q9PZS4	Q9PZS4	human cytom
241	5	10.2	131	8	Q9T9F1	Q9T9F1	gerris nepa	314	5	10.2	175	14	Q9PZS0	Q9PZS0	human cytom
242	5	10.2	131	8	Q9T9E8	Q9T9E8	aquarius pa	315	5	10.2	175	14	Q9PZR7	Q9PZR7	human cytom
243	5	10.2	131	8	Q9T9E7	Q9T9E7	aquarius pa	316	5	10.2	175	14	Q9PZR6	Q9PZR6	human cytom
244	5	10.2	131	8	Q9T9E6	Q9T9E6	aquarius el	317	5	10.2	175	14	Q9PZR4	Q9PZR4	human cytom
245	5	10.2	131	8	Q9T9E5	Q9T9E5	aquarius el	318	5	10.2	175	14	Q9PZR3	Q9PZR3	human cytom
246	5	10.2	131	8	Q9T9E1	Q9T9E1	limnogonus	319	5	10.2	175	14	Q9PZR1	Q9PZR1	human cytom
247	5	10.2	131	8	Q9T664	Q9T664	tenagognus	320	5	10.2	175	14	Q9PZR0	Q9PZR0	human cytom
248	5	10.2	131	8	Q9T434	Q9T434	gerris lati	321	5	10.2	175	14	Q9PZQ9	Q9PZQ9	human cytom
249	5	10.2	131	8	Q9T320	Q9T320	gerris insu	322	5	10.2	175	14	Q9PZQ8	Q9PZQ8	human cytom
250	5	10.2	132	5	Q9XWL2	Q9XWL2	caenorhabdi	323	5	10.2	175	14	Q9PZQ6	Q9PZQ6	human cytom
251	5	10.2	133	8	Q9MGJ7	Q9MGJ7	microtus lo	324	5	10.2	175	14	Q9PXA1	Q9PXA1	human cytom
252	5	10.2	134	5	Q9YX3	Q9YX3	hydra magni	325	5	10.2	175	14	Q9PX94	Q9PX94	human cytom
253	5	10.2	134	9	Q9T157	Q9T157	bacterioph	326	5	10.2	175	14	Q9PWY0	Q9PWY0	human cytom
254	5	10.2	136	8	Q9MGJ9	Q9MGJ9	microtus lo	327	5	10.2	175	14	Q9PWX3	Q9PWX3	human cytom
255	5	10.2	136	8	Q9MGJ8	Q9MGJ8	microtus lo	328	5	10.2	175	14	Q9XLD3	Q9XLD3	briemomyrus
256	5	10.2	136	8	Q9MGJ6	Q9MGJ6	microtus lo	329	5	10.2	177	9	Q80191	Q80191	methanobact
257	5	10.2	136	8	Q9MEZ1	Q9MEZ1	microtus lo	330	5	10.2	178	2	Q9Z5J3	Q9Z5J3	mycobacteri
258	5	10.2	136	8	Q9MDJ6	Q9MDJ6	microtus lo	331	5	10.2	178	2	Q9RN30	Q9RN30	bacillus an
259	5	10.2	136	14	Q65416	Q65416	beet curly	332	5	10.2	178	2	Q9JZ22	Q9JZ22	neisseria m
260	5	10.2	139	4	Q9NTB6	Q9NTB6	homo sapien	333	5	10.2	178	10	Q42461	Q42461	canavalia g
261	5	10.2	141	8	Q9N814	Q9N814	ixodes hexa	334	5	10.2	178	10	Q42492	Q42492	canavalia g
262	5	10.2	142	2	Q9S0F8	Q9S0F8	borrelia bu	335	5	10.2	178	10	Q9SLD4	Q9SLD4	arabidopsis
263	5	10.2	142	2	Q9R3Z2	Q9R3Z2	borrelia bu	336	5	10.2	180	8	Q9XQ15	Q9XQ15	nuphar adve
264	5	10.2	143	5	Q9W340	Q9W340	drosofila	337	5	10.2	181	8	Q9MIB7	Q9MIB7	mabuaya affi
265	5	10.2	143	8	Q9TLV3	Q9TLV3	cyanidium c	338	5	10.2	181	10	Q9LYH4	Q9LYH4	arabidopsis
266	5	10.2	143	10	Q9SMU5	Q9SMU5	arabidopsis	339	5	10.2	182	1	Q29054	Q29054	archaeoglob
267	5	10.2	143	10	Q9M0E2	Q9M0E2	arabidopsis	340	5	10.2	185	8	Q9ZZK9	Q9ZZK9	urosauros m
268	5	10.2	143	14	Q64804	Q64804	autographa	341	5	10.2	185	8	Q9ZZK8	Q9ZZK8	petrosaurus
269	5	10.2	144	2	Q9KJF4	Q9KJF4	thauera aro	342	5	10.2	185	8	Q9ZZK7	Q9ZZK7	uta palmeri
270	5	10.2	146	2	Q9K7A1	Q9K7A1	bacillus ha	343	5	10.2	185	8	Q9ZZK6	Q9ZZK6	uta stellat
271	5	10.2	154	5	Q15825	Q15825	euplotes oc	344	5	10.2	185	8	Q9ZZK5	Q9ZZK5	uta squamat
272	5	10.2	154	5	Q9VHN3	Q9VHN3	drosofila	345	5	10.2	185	8	Q9ZZK4	Q9ZZK4	uta antiqua
273	5	10.2	155	5	Q61977	Q61977	caenorhabdi	346	5	10.2	185	8	Q9ZZK3	Q9ZZK3	uta stansbu
274	5	10.2	157	8	Q9T245	Q9T245	phytophthor	347	5	10.2	185	8	Q9ZZK2	Q9ZZK2	uta stejnueg
275	5	10.2	158	5	Q23981	Q23981	drosofila	348	5	10.2	185	8	Q9XQ13	Q9XQ13	nuphar orbi
276	5	10.2	159	5	Q62289	Q62289	caenorhabdi	349	5	10.2	185	8	Q9T520	Q9T520	uta stansbu
277	5	10.2	159	5	Q9U238	Q9U238	caenorhabdi	350	5	10.2	185	8	Q9T519	Q9T519	uta stansbu
278	5	10.2	159	6	Q9N1N1	Q9N1N1	papio hamad	351	5	10.2	185	8	Q9T518	Q9T518	uta stansbu
279	5	10.2	160	6	Q9N1K0	Q9N1K0	macaca sylv	352	5	10.2	185	8	Q9T517	Q9T517	uta stansbu
280	5	10.2	160	14	Q73150	Q73150	human immun	353	5	10.2	185	8	Q9T516	Q9T516	uta stansbu
281	5	10.2	162	10	Q42410	Q42410	arabidopsis	354	5	10.2	185	8	Q9T515	Q9T515	uta stansbu
282	5	10.2	162	10	Q9L7F3	Q9L7F3	arabidopsis	355	5	10.2	185	8	Q9T514	Q9T514	uta stansbu
283	5	10.2	162	14	Q73147	Q73147	human immun	356	5	10.2	185	8	Q9T513	Q9T513	uta stansbu
284	5	10.2	162	14	Q73148	Q73148	human immun	357	5	10.2	185	8	Q9T512	Q9T512	uta stansbu
285	5	10.2	164	10	Q9SP66	Q9SP66	arabidopsis	358	5	10.2	185	8	Q9T511	Q9T511	uta stansbu
286	5	10.2	166	1	Q59236	Q59236	pyrococcus	359	5	10.2	185	8	Q9T510	Q9T510	uta stansbu
287	5	10.2	166	5	Q9VXR8	Q9VXR8	drosofila	360	5	10.2	185	8	Q9T509	Q9T509	uta stansbu
288	5	10.2	167	2	Q67858	Q67858	aquifex aeo	361	5	10.2	185	8	Q9T3A3	Q9T3A3	uta stansbu
289	5	10.2	167	3	Q9P6L4	Q9P6L4	schizosacch	362	5	10.2	185	8	Q9T3A2	Q9T3A2	uta stansbu
290	5	10.2	167	8	Q9P6L4	Q9P6L4	schizosacch	363	5	10.2	185	8	Q9MFR7	Q9MFR7	xenopoecilu
291	5	10.2	167	8	Q3371	Q3371	caretta car	364	5	10.2	186	8	Q9TCB3	Q9TCB3	nephrocelimi
292	5	10.2	167	8	Q33413	Q33413	dermochelys	365	5	10.2	186	9	Q9ZX69	Q9ZX69	mycobacteri
293	5	10.2	167	8	Q33442	Q33442	eretmochely	366	5	10.2	187	10	Q23132	Q23132	arabidopsis
294	5	10.2	167	8	Q33587	Q33587	lepidochely	367	5	10.2	188	5	Q9TXQ0	Q9TXQ0	caenorhabdi
295	5	10.2	167	8	Q33588	Q33588	lepidochely	368	5	10.2	189	8	Q9MFS8	Q9MFS8	oryzias cur
296	5	10.2	167	8	Q34068	Q34068	caretta car	369	5	10.2	190	2	Q9RMV0	Q9RMV0	bacillus an
297	5	10.2	167	8	Q34158	Q34158	chelonion my	370	5	10.2	190	2	Q9K284	Q9K284	streptomyce
298	5	10.2	167	8	Q34159	Q34159	chelonion my	371	5	10.2	191	2	Q9JVL1	Q9JVL1	neisseria m
299	5	10.2	167	8	Q34896	Q34896	lepidochely	372	5	10.2	191	5	Q9V8X3	Q9V8X3	drosofila
300	5	10.2	167	8	Q36595	Q36595	nator dep	373	5	10.2	191	8	Q9XLD3	Q9XLD3	macaca neme
301	5	10.2	167	8	Q31754	Q31754	chelydra se	374	5	10.2	191	14	Q98543	Q98543	paramecium
302	5	10.2	169	10	Q9LFP1	Q9LFP1	pyrococcus	375	5	10.2	194	5	Q62425	Q62425	caenorhabdi
303	5	10.2	171	1	Q9V175	Q9V175	pyrococcus	376	5	10.2	194	8	Q34083	Q34083	coryphaena
304	5	10.2	172	2	Q54789	Q54789	streptococc	377	5	10.2	194	10	Q9MOM9	Q9MOM9	arabidopsis
305	5	10.2	173	11	Q9JKD5	Q9JKD5	rattus norv	378	5	10.2	196	8	Q9XLC2	Q9XLC2	gymnarchus
306	5	10.2	174	10	Q39217	Q39217	arabidopsis	379	5	10.2	196	8	Q9XLB2	Q9XLB2	marcusenlus
307	5	10.2	175	4	Q9N285	Q9N285	homo sapien	380	5	10.2	196	8	Q9XLB1	Q9XLB1	pollimyrus
308	5	10.2	175	14	Q9WPM2	Q9WPM2	human cytom	381	5	10.2	196	8	Q9XLA6	Q9XLA6	ivindomyrus
309	5	10.2	175	14	Q9PZS8	Q9PZS8	human cytom	382	5	10.2	196	8	Q9XLA5	Q9XLA5	boulengerom
310	5	10.2	175	14	Q9PZS7	Q9PZS7	human cytom	383	5	10.2	198	2	Q9RCR0	Q9RCR0	streptococc
311	5	10.2	175	14	Q9PZS6	Q9PZS6	human cytom	384	5	10.2	198	2	Q9RCQ5	Q9RCQ5	streptococc

385	5	10.2	198	2	Q9RCQ2	Q9rcq2 streptococc	458	5	10.2	216	8	Q9TAG4	Q9tag4 uma exsul.
386	5	10.2	198	2	Q9RCP8	Q9rcp8 streptococc	459	5	10.2	216	8	Q9TAG3	Q9tag3 uma paraphy
387	5	10.2	198	2	Q9R2M1	Q9r2m1 streptococc	460	5	10.2	217	8	Q9XMK7	Q9xm7 ochotona pr
388	5	10.2	198	10	Q9LWB5	Q9lwb5 spinacia ol	461	5	10.2	217	8	Q9TH74	Q9th74 acomys mino
389	5	10.2	199	5	P91464	P91464 caenorhabdi	462	5	10.2	217	8	Q9TAH4	Q9tah4 uta stansbu
390	5	10.2	199	8	Q35995	Q35995 tetrapurtus	463	5	10.2	217	8	Q9TAH3	Q9tah3 urosaurus o
391	5	10.2	200	2	Q9RG41	Q9rg41 streptococc	464	5	10.2	217	8	Q9TAH2	Q9tah2 phrynosoma
392	5	10.2	201	2	Q9WYN5	Q9wyn5 thermotoga	465	5	10.2	217	8	Q9TAH1	Q9tah1 phrynosoma
393	5	10.2	201	6	Q9TT21	Q9tt21 bos taurus	466	5	10.2	217	8	Q9TAH0	Q9tah0 seeloporus
394	5	10.2	201	10	Q9MLA0	Q9mla0 arabidopsis	467	5	10.2	217	8	Q9TAG9	Q9tag9 callisaurus
395	5	10.2	202	5	Q20534	Q20534 caenorhabdi	468	5	10.2	217	8	Q9TAG8	Q9tag8 callisaurus
396	5	10.2	202	8	Q9MFT0	Q9mft0 oryzias car	469	5	10.2	217	8	Q9TAG7	Q9tag7 cophosaurus
397	5	10.2	202	8	Q9MFS1	Q9mfs1 oryzias mek	470	5	10.2	217	8	Q9TAG6	Q9tag6 cophosaurus
398	5	10.2	202	10	Q9LW58	Q9lw58 arabidopsis	471	5	10.2	217	8	Q9TAG5	Q9tag5 uma inornat
399	5	10.2	203	2	Q9XBL4	Q9xbl4 bacillus ce	472	5	10.2	217	8	Q9TAG2	Q9tag2 holbrookia
400	5	10.2	203	2	Q9L305	Q9l3q5 eubacterium	473	5	10.2	217	8	Q9TAG1	Q9tag1 holbrookia
401	5	10.2	203	8	Q36241	Q36241 xiphias gla	474	5	10.2	217	8	Q9TAG0	Q9tag0 holbrookia
402	5	10.2	203	8	Q35978	Q35978 tetrapurtus	475	5	10.2	217	8	Q9TAF9	Q9taf9 holbrookia
403	5	10.2	203	8	Q35979	Q35979 tetrapurtus	476	5	10.2	217	8	Q9TAF8	Q9taf8 holbrookia
404	5	10.2	203	8	Q35979	Q34819 istiophorus	477	5	10.2	217	8	Q9TAF7	Q9taf7 holbrookia
405	5	10.2	203	8	Q35008	Q35008 makaira ind	478	5	10.2	217	8	Q9TAF6	Q9taf6 holbrookia
406	5	10.2	203	8	Q35049	Q35049 tetrapurtus	479	5	10.2	217	8	Q9TAF5	Q9taf5 holbrookia
407	5	10.2	203	8	Q35049	Q35049 makaira nig	480	5	10.2	217	8	Q9TAF4	Q9taf4 holbrookia
408	5	10.2	203	8	Q9MLU9	Q9mlu9 bolitogloss	481	5	10.2	217	8	Q9TAF3	Q9taf3 holbrookia
409	5	10.2	203	8	Q9MLU6	Q9mlu6 bolitogloss	482	5	10.2	217	8	Q9TAF2	Q9taf2 holbrookia
410	5	10.2	203	8	Q9MLB5	Q9mlb5 mabuya eleg	483	5	10.2	217	8	Q9TAF0	Q9taf0 callisaurus
411	5	10.2	203	10	Q9STJ2	Q9stj2 arabidopsis	484	5	10.2	217	8	Q9T454	Q9t454 uma scopari
412	5	10.2	204	8	Q36105	Q36105 tetrapurtus	485	5	10.2	217	8	Q9T3Y7	Q9t3y7 uma notata.
413	5	10.2	204	8	Q9MLU1	Q9mlu1 bolitogloss	486	5	10.2	218	2	Q9KKC0	Q9kkc0 borrelia he
414	5	10.2	204	8	Q9MFS6	Q9mfs6 oryzias jav	487	5	10.2	219	8	Q9XLM9	Q9xlm9 chaicporus
415	5	10.2	206	8	Q9MLT9	Q9mlt9 bolitogloss	488	5	10.2	219	8	Q9TAU5	Q9tau5 strongylura
416	5	10.2	206	10	Q9MOW0	Q9mow0 bolitogloss	489	5	10.2	219	8	Q9MM62	Q9mm62 adolfus vau
417	5	10.2	207	8	Q9MLB8	Q9mlb8 arabidopsis	490	5	10.2	219	8	Q9MM61	Q9mm61 eremias vel
418	5	10.2	207	8	Q9MLB4	Q9mlb4 mabuya macu	491	5	10.2	220	2	Q9ZKA5	Q9zka5 nucras tess
419	5	10.2	207	8	Q9MDY2	Q9mdy2 bolitogloss	492	5	10.2	220	2	Q9ZKA5	Q9zka5 helicobacte
420	5	10.2	208	5	Q9W951	Q9w951 drosophila	493	5	10.2	220	8	Q9T2Y6	Q9t2y6 strongylura
421	5	10.2	209	8	Q9XLV1	Q9xlv1 bolitogloss	494	5	10.2	220	8	Q9T2Y6	Q9t2y6 strongylura
422	5	10.2	210	8	Q99906	Q99906 potamotrygo	495	5	10.2	222	8	Q34402	Q34402 mabuya quin
423	5	10.2	210	8	Q9W553	Q9w553 carduelis c	496	5	10.2	222	8	Q34486	Q34486 euproctus m
424	5	10.2	210	8	Q9MFS9	Q9mfs9 oryzias cel	497	5	10.2	222	8	Q34492	Q34492 euproctus p
425	5	10.2	210	8	Q9MFS3	Q9mfs3 oryzias lat	498	5	10.2	222	8	Q35696	Q35696 pleurodeles
426	5	10.2	210	8	Q9MFS3	Q9mfs3 oryzias luz	499	5	10.2	223	1	Q36182	Q36182 triturus vu
427	5	10.2	210	8	Q9MFS2	Q9mfs2 oryzias mar	500	5	10.2	223	2	Q9RME7	Q9rme7 zymomonas m
428	5	10.2	210	8	Q9MFS0	Q9mfs0 oryzias nig	501	5	10.2	224	8	Q9XMK6	Q9xm6 sylviagus
429	5	10.2	210	8	Q9MFR9	Q9mfr9 oryzias nig	502	5	10.2	224	8	Q9TAU3	Q9tau3 pseudotylus
430	5	10.2	210	8	Q9MFR8	Q9mfr8 xenopoecili	503	5	10.2	224	8	Q9TAU2	Q9tau2 pseudotylus
431	5	10.2	211	8	Q9MFS5	Q9mfs5 oryzias jav	504	5	10.2	224	8	Q9T346	Q9t346 pseudotylus
432	5	10.2	212	10	Q9LWF7	Q9lwf7 oryza sativ	505	5	10.2	224	8	Q9TAU1	Q9tau1 pseudotylus
433	5	10.2	214	2	Q67790	Q67790 aquifex aeo	506	5	10.2	224	8	Q9T346	Q9t346 pseudotylus
434	5	10.2	214	2	P73763	P73763 synechocyst	507	5	10.2	225	8	Q9TAU6	Q9tau6 belonion ap
435	5	10.2	214	8	Q9T554	Q9t554 carduelis c	508	5	10.2	225	8	Q9MIB6	Q9mib6 mabuya cf.
436	5	10.2	214	8	Q9MLU5	Q9mlu5 bolitogloss	509	5	10.2	226	4	Q9KNV6	Q9knv6 vibrio chol
437	5	10.2	214	8	Q9MLU2	Q9mlu2 bolitogloss	510	5	10.2	226	5	Q16018	Q16018 homo sapien
438	5	10.2	215	5	Q20614	Q20614 caenorhabdi	511	5	10.2	226	8	Q9TAV1	Q9tav1 caenorhabdi
439	5	10.2	215	8	Q34237	Q34237 capricornis	512	5	10.2	226	14	Q9R686	Q9r686 simian cyto
440	5	10.2	215	8	Q34238	Q34238 capricornis	513	5	10.2	227	5	Q00924	Q00924 plasmodium
441	5	10.2	215	8	Q35152	Q35152 nemorhaedus	514	5	10.2	227	8	Q34432	Q34432 ensatina es
442	5	10.2	215	8	Q35206	Q35206 oreomys am	515	5	10.2	227	8	Q34433	Q34433 ensatina es
443	5	10.2	215	8	Q35744	Q35744 rupicapra r	516	5	10.2	227	8	Q34434	Q34434 ensatina es
444	5	10.2	215	8	Q34872	Q34872 oryctolagus	517	5	10.2	227	8	Q34435	Q34435 ensatina es
445	5	10.2	215	8	Q9MLV2	Q9mlv2 bolitogloss	518	5	10.2	227	8	Q34437	Q34437 ensatina es
446	5	10.2	215	8	Q9MLV1	Q9mlv1 bolitogloss	519	5	10.2	227	8	Q34438	Q34438 ensatina es
447	5	10.2	215	8	Q9MLV0	Q9mlv0 bolitogloss	520	5	10.2	227	8	Q34439	Q34439 ensatina es
448	5	10.2	215	8	Q9MLU3	Q9mlu3 bolitogloss	521	5	10.2	227	8	Q34440	Q34440 ensatina es
449	5	10.2	215	8	Q9MLU0	Q9mlu0 bolitogloss	522	5	10.2	227	8	Q34441	Q34441 ensatina es
450	5	10.2	215	8	Q9MLU3	Q9mlu3 bolitogloss	523	5	10.2	227	8	Q34442	Q34442 ensatina es
451	5	10.2	215	8	Q9MLU0	Q9mlu0 bolitogloss	524	5	10.2	227	8	Q34443	Q34443 ensatina es
452	5	10.2	215	8	Q9MLT8	Q9mlt8 bolitogloss	525	5	10.2	227	8	Q34444	Q34444 ensatina es
453	5	10.2	215	8	Q9MLT5	Q9mlt5 bolitogloss	526	5	10.2	227	8	Q34445	Q34445 ensatina es
454	5	10.2	215	8	Q9MBC5	Q9mbc5 bolitogloss	527	5	10.2	227	8	Q34446	Q34446 ensatina es
455	5	10.2	215	8	Q9MDQ2	Q9mdq2 bolitogloss	528	5	10.2	227	8	Q34446	Q34446 ensatina es
456	5	10.2	216	2	Q9PBU7	Q9pbu7 xylella fas	529	5	10.2	227	8	Q34446	Q34446 ensatina es
457	5	10.2	216	8	Q36007	Q36007 triturus ca	530	5	10.2	227	8	Q34448	Q34448 ensatina es

531	5	10.2	227	8	Q34449	Q34449 ensatina es	604	5	10.2	238	2	P72818	P72818 synechocyst
532	5	10.2	227	8	Q34450	Q34450 ensatina es	605	5	10.2	238	8	Q03377	Q03377 aryanomys
533	5	10.2	227	8	Q34451	Q34451 ensatina es	606	5	10.2	238	10	Q02901	Q02901 arabidopsis
534	5	10.2	227	8	Q34452	Q34452 ensatina es	607	5	10.2	239	5	Q17769	Q17769 caenorhabdi
535	5	10.2	227	8	Q34453	Q34453 ensatina es	608	5	10.2	239	10	Q98IH3	Q98IH3 arabidopsis
536	5	10.2	227	8	Q35427	Q35427 plethodon e	609	5	10.2	240	2	Q49014	Q49014 mycoplasma
537	5	10.2	228	1	Q9UXX2	Q9UXX2 pyrococcus	610	5	10.2	242	2	Q25560	Q25560 helicobacte
538	5	10.2	228	8	Q9XLV7	Q9XLV7 dasytyllus r	611	5	10.2	242	2	Q92KU8	Q92KU8 helicobacte
539	5	10.2	228	8	Q9XLV6	Q9XLV6 dasytyllus a	612	5	10.2	243	2	Q69830	Q69830 streptomyc
540	5	10.2	228	8	Q9XLV5	Q9XLV5 dasytyllus m	613	5	10.2	243	14	Q09502	Q09502 garlic viru
541	5	10.2	228	8	Q9XLV4	Q9XLV4 dasytyllus c	614	5	10.2	244	8	Q34293	Q34293 dasyatis ak
542	5	10.2	228	8	Q9XLV2	Q9XLV2 dasytyllus m	615	5	10.2	244	8	Q35520	Q35520 pristicis per
543	5	10.2	228	8	Q9XLV0	Q9XLV0 dasytyllus t	616	5	10.2	244	8	Q35720	Q35720 rhinobatos
544	5	10.2	228	8	Q9XLU9	Q9XLU9 chromis chr	617	5	10.2	244	8	Q35892	Q35892 squatina ne
545	5	10.2	228	8	Q9TAU7	Q9TAU7 belonion di	618	5	10.2	244	10	Q9LV08	Q9LV08 arabidopsis
546	5	10.2	228	8	Q9MR8	Q9MR8 hemidactylu	619	5	10.2	245	8	Q63703	Q63703 batrachosep
547	5	10.2	228	8	Q9MR7	Q9MR7 pachydactyl	620	5	10.2	247	5	Q01646	Q01646 drosophila
548	5	10.2	228	8	Q9MR6	Q9MR6 tarentola a	621	5	10.2	247	13	Q9IH93	Q9IH93 brachydanio
549	5	10.2	228	8	Q9MR5	Q9MR5 tarentola b	622	5	10.2	247	14	P87516	P87516 bovine rota
550	5	10.2	228	8	Q9MR4	Q9MR4 tarentola b	623	5	10.2	247	14	P87517	P87517 bovine rota
551	5	10.2	228	8	Q9MR3	Q9MR3 tarentola b	624	5	10.2	247	14	P87518	P87518 bovine rota
552	5	10.2	228	8	Q9MR2	Q9MR2 tarentola b	625	5	10.2	247	14	Q9WAT1	Q9WAT1 bovine grou
553	5	10.2	228	8	Q9MR1	Q9MR1 tarentola d	626	5	10.2	248	3	Q74926	Q74926 schizosacch
554	5	10.2	228	8	Q9MHQ6	Q9MHQ6 tarentola g	627	5	10.2	248	5	Q27458	Q27458 botryllus s
555	5	10.2	228	8	Q9MHQ5	Q9MHQ5 tarentola g	628	5	10.2	249	8	Q9TDQ4	Q9TDQ4 muntiacus f
556	5	10.2	228	8	Q9MHQ4	Q9MHQ4 tarentola g	629	5	10.2	249	8	Q9TDQ3	Q9TDQ3 muntiacus c
557	5	10.2	228	8	Q9MHP7	Q9MHP7 tarentola c	630	5	10.2	250	2	P72645	P72645 synechocyst
558	5	10.2	228	8	Q9MHP6	Q9MHP6 tarentola c	631	5	10.2	250	8	Q9TAV6	Q9TAV6 potamorhaph
559	5	10.2	228	8	Q9MHP5	Q9MHP5 tarentola d	632	5	10.2	250	8	Q9TAV5	Q9TAV5 potamorhaph
560	5	10.2	228	8	Q9MHP4	Q9MHP4 tarentola d	633	5	10.2	250	8	Q9TAV4	Q9TAV4 potamorhaph
561	5	10.2	228	8	Q9MHP3	Q9MHP3 tarentola d	634	5	10.2	250	8	Q9TAV3	Q9TAV3 potamorhaph
562	5	10.2	228	8	Q9MHP2	Q9MHP2 tarentola d	635	5	10.2	250	8	Q9TAV2	Q9TAV2 potamorhaph
563	5	10.2	228	8	Q9MHP1	Q9MHP1 tarentola d	636	5	10.2	250	8	Q9TAV0	Q9TAV0 potamorhaph
564	5	10.2	228	8	Q9MHP0	Q9MHP0 tarentola d	637	5	10.2	250	8	Q9TAF3	Q9TAF3 potamorhaph
565	5	10.2	228	8	Q9MHN9	Q9MHN9 tarentola d	638	5	10.2	250	8	Q9T474	Q9T474 potamorhaph
566	5	10.2	228	8	Q9MHN8	Q9MHN8 tarentola d	639	5	10.2	250	8	Q9T3P2	Q9T3P2 potamorhaph
567	5	10.2	228	8	Q9MHN7	Q9MHN7 tarentola d	640	5	10.2	250	8	Q9T3H3	Q9T3H3 potamorhaph
568	5	10.2	228	8	Q9ME85	Q9ME85 tarentola b	641	5	10.2	251	8	Q63704	Q63704 batrachosep
569	5	10.2	228	8	Q9MDR2	Q9MDR2 tarentola b	642	5	10.2	251	8	Q63707	Q63707 batrachosep
570	5	10.2	228	8	Q9MDN3	Q9MDN3 tarentola c	643	5	10.2	251	11	P70331	P70331 mus musculu
571	5	10.2	228	8	Q9MDG4	Q9MDG4 tarentola c	644	5	10.2	251	14	Q67693	Q67693 garlic viru
572	5	10.2	228	8	Q9MDF7	Q9MDF7 tarentola c	645	5	10.2	252	8	Q99908	Q99908 potamotrygo
573	5	10.2	228	8	Q9MDE2	Q9MDE2 tarentola r	646	5	10.2	252	10	Q9SJB2	Q9SJB2 arabidopsis
574	5	10.2	228	10	Q43308	Q43308 arabidopsis	647	5	10.2	252	14	O12299	O12299 garlic mite
575	5	10.2	229	2	O51423	O51423 borrelia bu	648	5	10.2	253	2	Q32833	Q32833 lactobacill
576	5	10.2	229	2	Q32821	Q32821 legionella	649	5	10.2	253	14	O40643	O40643 salmireline
577	5	10.2	229	8	Q9TBQ2	Q9TBQ2 amphistichu	650	5	10.2	254	1	Q58498	Q58498 methanococc
578	5	10.2	229	8	Q9TBQ1	Q9TBQ1 brachyistiu	651	5	10.2	254	5	Q9VM7	Q9VM7 drosophila
579	5	10.2	229	8	Q9TBQ0	Q9TBQ0 cymatogaste	652	5	10.2	254	5	Q9V3J2	Q9V3J2 drosophila
580	5	10.2	229	8	Q9TBP9	Q9TBP9 rhacotocula	653	5	10.2	254	8	Q63705	Q63705 batrachosep
581	5	10.2	229	8	Q9TBP8	Q9TBP8 embiotoca j	654	5	10.2	255	8	Q63706	Q63706 batrachosep
582	5	10.2	229	8	Q9TBP7	Q9TBP7 hyperprosop	655	5	10.2	255	8	Q99904	Q99904 dasyatis ha
583	5	10.2	229	8	Q9TBP6	Q9TBP6 hysterothorp	656	5	10.2	255	8	Q99905	Q99905 urobatis ha
584	5	10.2	229	8	Q9TBP5	Q9TBP5 rhacotocula	657	5	10.2	255	8	Q99907	Q99907 potamotrygo
585	5	10.2	229	8	Q9TBP4	Q9TBP4 hypsirus ca	658	5	10.2	255	8	Q99909	Q99909 potamotrygo
586	5	10.2	229	8	Q9TBP3	Q9TBP3 micrometrus	659	5	10.2	255	8	Q99911	Q99911 taenlura ly
587	5	10.2	229	8	Q9TBP2	Q9TBP2 phanerodon	660	5	10.2	255	8	Q99912	Q99912 gymmura mac
588	5	10.2	229	8	Q9TBP1	Q9TBP1 zalembius r	661	5	10.2	255	8	Q99913	Q99913 dasyatis lo
589	5	10.2	229	8	Q9TBP0	Q9TBP0 ditrema tem	662	5	10.2	255	8	Q99914	Q99914 myliobatis
590	5	10.2	229	8	Q9TBN9	Q9TBN9 neoditrema	663	5	10.2	255	8	Q99915	Q99915 rhinoptera
591	5	10.2	229	8	Q9TAU8	Q9TAU8 potamorhaph	664	5	10.2	255	8	Q99916	Q99916 mobula thur
592	5	10.2	230	2	Q9R716	Q9R716 agrobacteri	665	5	10.2	255	8	Q99917	Q99917 plesiotrygo
593	5	10.2	230	2	Q9R699	Q9R699 agrobacteri	666	5	10.2	255	8	Q99918	Q99918 himantura g
594	5	10.2	231	2	Q9RWE4	Q9RWE4 agrobacteri	667	5	10.2	255	8	Q99919	Q99919 himantura p
595	5	10.2	232	2	O31050	O31050 streptococc	668	5	10.2	255	8	Q99920	Q99920 himantura s
596	5	10.2	232	10	Q9MOM3	Q9MOM3 arabidopsis	669	5	10.2	256	2	O68612	O68612 synechococ
597	5	10.2	233	2	O56749	O56749 wolinnella s	670	5	10.2	257	5	Q9VH58	Q9VH58 drosophila
598	5	10.2	233	2	Q9KVJ5	Q9KVJ5 vibrio chol	671	5	10.2	257	8	Q9TEU5	Q9TEU5 apalone spi
599	5	10.2	235	8	Q9TAU9	Q9TAU9 potamorhaph	672	5	10.2	257	8	Q9TEU4	Q9TEU4 apalone spi
600	5	10.2	236	6	Q9N703	Q9N703 cercopitheo	673	5	10.2	257	8	Q9TEU3	Q9TEU3 apalone spi
601	5	10.2	236	6	Q9N039	Q9N039 saquinus oe	674	5	10.2	257	8	Q9TEU2	Q9TEU2 apalone fer
602	5	10.2	236	11	O62745	O62745 rattus norv	675	5	10.2	257	8	Q9TEU1	Q9TEU1 apalone fer
603	5	10.2	237	8	Q9MM63	Q9MM63 lacerta pat	676	5	10.2	257	8	Q9TEU0	Q9TEU0 apalone mut

677	5	10.2	257	8	Q9TEH9	Q9tet9 apalone mut	750	5	10.2	290	8	Q9TEJ1	Q9tet1 eutropius d
678	5	10.2	257	8	Q9TEH8	Q9tet8 apalone mut	751	5	10.2	292	2	Q9RS12	Q9rs12 deinococcus
679	5	10.2	257	8	Q9T4S7	Q9t4s7 apalone mut	752	5	10.2	292	3	Q9P4C1	Q9p4c1 kluyveromyc
680	5	10.2	257	8	Q9T448	Q9t448 apalone spi	753	5	10.2	294	4	Q9NW22	Q9nw22 homo sapien
681	5	10.2	257	8	Q9T3X6	Q9t3x6 apalone spi	754	5	10.2	295	2	Q54097	Q54097 streptomyce
682	5	10.2	257	8	Q9T3M6	Q9t3m6 apalone spi	755	5	10.2	295	8	Q03320	Q03320 elseya lati
683	5	10.2	257	10	Q9LRL6	Q9lr16 arabidopsis	756	5	10.2	295	8	Q9TEJ5	Q9tej5 eutropius d
684	5	10.2	259	2	Q9KR23	Q9kr23 vibrio chol	757	5	10.2	295	8	Q9TEJ3	Q9tej3 eutropius d
685	5	10.2	259	4	Q9Y5B2	Q9y5b2 homo sapien	758	5	10.2	296	5	Q19528	Q19528 caenorhabdi
686	5	10.2	259	8	Q48113	Q48113 ramphotyphi	759	5	10.2	296	8	Q9TEJ2	Q9tej2 eutropius d
687	5	10.2	259	10	Q9SGI3	Q9sg13 arabidopsis	760	5	10.2	297	5	Q17418	Q17418 caenorhabdi
688	5	10.2	259	14	Q98687	Q98687 simian cyto	761	5	10.2	297	5	Q9NFL9	Q9nfl9 globodera p
689	5	10.2	259	14	Q67661	Q67661 garlic mite	762	5	10.2	297	8	Q47824	Q47824 ocadia sine
690	5	10.2	261	8	Q48088	Q48088 hemidactylu	763	5	10.2	297	8	Q47825	Q47825 cuora auroc
691	5	10.2	262	5	Q9XU29	Q9xu29 caenorhabdi	764	5	10.2	297	8	Q03290	Q03290 clemmys mar
692	5	10.2	263	2	Q78174	Q78174 escherichia	765	5	10.2	297	8	Q03291	Q03291 chelonias my
693	5	10.2	263	4	Q9Y3S5	Q9y3s5 homo sapien	766	5	10.2	297	8	Q03292	Q03292 graptomys p
694	5	10.2	263	8	Q02673	Q02673 himatione s	767	5	10.2	297	8	Q03293	Q03293 geochelone
695	5	10.2	263	8	Q02674	Q02674 hemignathus	768	5	10.2	297	8	Q03294	Q03294 heosemys sp
696	5	10.2	263	8	Q02675	Q02675 vestliaria c	769	5	10.2	297	8	Q03295	Q03295 trachemys s
697	5	10.2	263	8	Q02676	Q02676 loxops cocc	770	5	10.2	297	8	Q03296	Q03296 apalone spi
698	5	10.2	263	8	Q02677	Q02677 oreomyctis	771	5	10.2	297	8	Q03301	Q03301 chelus fimb
699	5	10.2	263	8	Q02678	Q02678 paroreomyza	772	5	10.2	297	8	Q03305	Q03305 carettochel
700	5	10.2	263	8	Q02679	Q02679 hemignathus	773	5	10.2	297	8	Q03312	Q03312 chinemys re
701	5	10.2	263	8	Q02680	Q02680 palmeria do	774	5	10.2	297	8	Q03315	Q03315 chelydra se
702	5	10.2	263	8	Q02681	Q02681 pseudonesto	775	5	10.2	297	8	Q03316	Q03316 dermocheleys
703	5	10.2	263	8	Q02682	Q02682 oreomyctis	776	5	10.2	297	8	Q03317	Q03317 dermatemys
704	5	10.2	263	8	Q02683	Q02683 loxia curvi	777	5	10.2	297	8	Q03321	Q03321 kinosternon
705	5	10.2	263	8	Q02684	Q02684 carpodacus	778	5	10.2	297	8	Q03327	Q03327 podocnemis
706	5	10.2	264	8	Q9MM17	Q9mm17 stomatorhin	779	5	10.2	297	8	Q03328	Q03328 phrynosps gi
707	5	10.2	265	3	Q78794	Q78794 schizosacch	780	5	10.2	297	8	Q03335	Q03335 pelusios wi
708	5	10.2	265	3	Q74817	Q74817 schizosacch	781	5	10.2	297	8	Q03339	Q03339 staurotypos
709	5	10.2	265	5	Q9NGC5	Q9ngc5 dictyosteli	782	5	10.2	298	5	Q61736	Q61736 caenorhabdi
710	5	10.2	266	14	Q66793	Q66793 ectromelia	783	5	10.2	298	6	Q9XT56	Q9xt56 bos laurus
711	5	10.2	267	2	Q9KX70	Q9kx70 mycoplasma	784	5	10.2	299	2	Q49149	Q49149 methylobact
712	5	10.2	267	8	Q35149	Q35149 notiomys ed	785	5	10.2	299	4	Q9Y624	Q9y624 homo sapien
713	5	10.2	267	8	Q02951	Q02951 damaliscus	786	5	10.2	299	8	Q9THC4	Q9thc4 lemmus sibi
714	5	10.2	267	8	Q02950	Q02950 gazella gra	787	5	10.2	300	1	Q28459	Q28459 archaeoglob
715	5	10.2	267	14	Q87048	Q87048 semliki for	788	5	10.2	300	4	Q00121	Q00121 homo sapien
716	5	10.2	268	4	Q9UJ44	Q9uj44 homo sapien	789	5	10.2	300	8	Q02828	Q02828 sauromalus
717	5	10.2	268	1	Q95886	Q95886 sulfolobus	790	5	10.2	300	8	Q02829	Q02829 sauromalus
718	5	10.2	269	5	Q9VFA5	Q9vfa5 drosophila	791	5	10.2	300	8	Q02830	Q02830 sauromalus
719	5	10.2	269	14	Q41125	Q41125 paramacium	792	5	10.2	300	8	Q02831	Q02831 sauromalus
720	5	10.2	270	5	Q9N364	Q9n364 caenorhabdi	793	5	10.2	300	8	Q02832	Q02832 sauromalus
721	5	10.2	270	10	Q9LT67	Q9lt67 arabidopsis	794	5	10.2	300	8	Q02833	Q02833 sauromalus
722	5	10.2	271	8	Q9T3K5	Q9t3k5 gallotia si	795	5	10.2	300	8	Q02834	Q02834 sauromalus
723	5	10.2	271	8	Q9T3K4	Q9t3k4 gallotia si	796	5	10.2	300	8	Q02835	Q02835 sauromalus
724	5	10.2	272	2	Q45329	Q45329 brucella ov	797	5	10.2	300	8	Q02836	Q02836 sauromalus
725	5	10.2	273	3	Q9ZCC1	Q9zcc1 rickettsia	798	5	10.2	300	8	Q02837	Q02837 sauromalus
726	5	10.2	273	3	Q94670	Q94670 schizosacch	799	5	10.2	300	8	Q02838	Q02838 sauromalus
727	5	10.2	273	5	Q76688	Q76688 caenorhabdi	800	5	10.2	300	8	Q02839	Q02839 sauromalus
728	5	10.2	274	2	Q9PNE8	Q9pne8 campylobact	801	5	10.2	300	8	Q02840	Q02840 sauromalus
729	5	10.2	274	3	Q04396	Q04396 saccharomyc	802	5	10.2	300	8	Q02841	Q02841 sauromalus
730	5	10.2	275	1	Q28963	Q28963 archaeoglob	803	5	10.2	300	8	Q02842	Q02842 sauromalus
731	5	10.2	275	5	Q9VZB9	Q9vzb9 drosophila	804	5	10.2	300	8	Q02843	Q02843 sauromalus
732	5	10.2	275	10	Q9SAJ8	Q9saj8 arabidopsis	805	5	10.2	300	8	Q02844	Q02844 sauromalus
733	5	10.2	276	2	Q9S3R6	Q9s3r6 porphyromon	806	5	10.2	300	8	Q02845	Q02845 sauromalus
734	5	10.2	276	3	Q36033	Q36033 schizosacch	807	5	10.2	300	8	Q02846	Q02846 sauromalus
735	5	10.2	276	5	Q9VFE6	Q9vfe6 drosophila	808	5	10.2	300	8	Q02847	Q02847 ctenosaura
736	5	10.2	276	8	Q9MM44	Q9mm44 brienomyrus	809	5	10.2	300	8	Q02848	Q02848 cyclura nub
737	5	10.2	279	2	Q9X1F1	Q9x1f1 thermotoga	810	5	10.2	300	8	Q02849	Q02849 dipsosaurus
738	5	10.2	279	5	Q21964	Q21964 caenorhabdi	811	5	10.2	300	8	Q02850	Q02850 conolophus
739	5	10.2	282	1	Q58835	Q58835 methanococc	812	5	10.2	300	8	Q21739	Q21739 sauromalus
740	5	10.2	283	10	Q9SJB6	Q9sjb6 arabidopsis	813	5	10.2	300	8	Q21771	Q21771 sauromalus
741	5	10.2	284	5	Q9W3P6	Q9w3p6 drosophila	814	5	10.2	300	8	Q21776	Q21776 sauromalus
742	5	10.2	284	14	Q42087	Q42087 equine herp	815	5	10.2	300	8	Q21779	Q21779 sauromalus
743	5	10.2	285	4	Q9KMC9	Q9kmc9 vibrio chol	816	5	10.2	300	8	Q33966	Q33966 brachylophu
744	5	10.2	285	4	Q43608	Q43608 homo sapien	817	5	10.2	300	8	Q9THC5	Q9thc5 lemmus sibi
745	5	10.2	285	8	P92814	P92814 paralichthy	818	5	10.2	300	11	Q88792	Q88792 mus musculu
746	5	10.2	286	2	Q9R640	Q9r640 mycobacteri	819	5	10.2	300	11	Q9JHY1	Q9jhy1 rattus norv
747	5	10.2	286	5	Q18004	Q18004 caenorhabdi	820	5	10.2	302	2	Q9X9Y3	Q9x9y3 streptomyce
748	5	10.2	286	5	Q9U0J8	Q9u0j8 plasmodium d	821	5	10.2	302	3	P87106	P87106 pneumocysti
749	5	10.2	290	8	Q9TEJ4	Q9tej4 eutropius d	822	5	10.2	302	3	Q04110	Q04110 saccharomyc

823	5	10.2	302	5	Q21937	Q21937 caenorhabdi	896	5	10.2	332	2	P71945	P71945 mycobacteri
824	5	10.2	303	8	Q92ZV2	Q92ZV2 lemmus trim	897	5	10.2	332	2	Q9JUW5	Q9JUW5 neisseria m
825	5	10.2	303	10	Q9XTH1	Q9XTH1 arabidopsis	898	5	10.2	332	10	Q9M510	Q9M510 lycopersico
826	5	10.2	304	2	Q9PJ91	Q9PJ91 campylobact	899	5	10.2	332	10	Q9LUA2	Q9LUA2 arabidopsis
827	5	10.2	304	5	Q21579	Q21579 caenorhabdi	900	5	10.2	332	14	Q9Q8C1	Q9Q8C1 yaba monkey
828	5	10.2	304	10	Q22140	Q22140 arabidopsis	901	5	10.2	334	2	Q9PHS9	Q9PHS9 campylobact
829	5	10.2	304	10	Q9LPY1	Q9LPY1 arabidopsis	902	5	10.2	335	2	Q9RGU4	Q9RGU4 salmonella
830	5	10.2	305	2	Q9PQ27	Q9PQ27 ureaplasma	903	5	10.2	335	4	Q9NZ56	Q9NZ56 homo sapien
831	5	10.2	305	8	Q92ZV6	Q92ZV6 lemmus sibi	904	5	10.2	335	8	Q03383	Q03383 trichechus
832	5	10.2	305	8	Q92ZV5	Q92ZV5 lemmus sibi	905	5	10.2	335	8	Q09233	Q09233 hydrotomali
833	5	10.2	305	8	Q92ZV4	Q92ZV4 lemmus sibi	906	5	10.2	335	8	Q92Y31	Q92Y31 elephantulu
834	5	10.2	305	8	Q92ZV3	Q92ZV3 lemmus trim	907	5	10.2	336	1	Q27597	Q27597 methanobact
835	5	10.2	305	8	Q92ZV1	Q92ZV1 lemmus sibi	908	5	10.2	336	2	Q51135	Q51135 borrelia bu
836	5	10.2	306	8	Q34412	Q34412 emoi caeru	909	5	10.2	336	3	Q94150	Q94150 candida alb
837	5	10.2	307	10	Q80577	Q80577 arabidopsis	910	5	10.2	336	8	Q79424	Q79424 neomys anom
838	5	10.2	308	9	Q38096	Q38096 bacterioph	911	5	10.2	336	8	Q9XMF1	Q9XMF1 acomys sp.
839	5	10.2	309	1	Q58333	Q58333 pyrococcus	912	5	10.2	336	8	Q9TH77	Q9TH77 acomys sp.
840	5	10.2	309	2	Q51695	Q51695 borrelia bu	913	5	10.2	337	10	Q9SGD1	Q9SGD1 arabidopsis
841	5	10.2	309	8	Q34413	Q34413 emoi caeru	914	5	10.2	337	14	Q55820	Q55820 rio bravo v
842	5	10.2	309	10	Q9SN79	Q9SN79 arabidopsis	915	5	10.2	340	2	Q9RDV6	Q9RDV6 mycoplasma
843	5	10.2	310	1	Q28615	Q28615 archaeoglob	916	5	10.2	340	5	Q23672	Q23672 caenorhabdi
844	5	10.2	310	2	Q45414	Q45414 bacillus sp	917	5	10.2	340	8	Q9TEE3	Q9TEE3 schilbe int
845	5	10.2	310	5	Q94389	Q94389 caenorhabdi	918	5	10.2	340	8	Q9SUX8	Q9SUX8 arabidopsis
846	5	10.2	311	5	Q9N768	Q9N768 leishmania	919	5	10.2	341	2	P72894	P72894 synechocyst
847	5	10.2	311	8	Q95789	Q95789 emoi caeru	920	5	10.2	341	5	Q9VT93	Q9VT93 drosophila
848	5	10.2	311	8	Q95790	Q95790 emoi caeru	921	5	10.2	341	5	Q9VR72	Q9VR72 drosophila
849	5	10.2	311	8	Q95791	Q95791 emoi caeru	922	5	10.2	342	3	Q9P5N5	Q9P5N5 neurospora
850	5	10.2	311	8	Q95792	Q95792 emoi caeru	923	5	10.2	342	8	Q9TEE2	Q9TEE2 schilbe int
851	5	10.2	311	8	Q95794	Q95794 emoi impar	924	5	10.2	343	10	Q9M519	Q9M519 populus alb
852	5	10.2	311	8	Q95795	Q95795 emoi impar	925	5	10.2	343	8	Q9MJT2	Q9MJT2 emys orbicu
853	5	10.2	311	8	Q95796	Q95796 emoi isola	926	5	10.2	345	8	Q9MJT1	Q9MJT1 emys orbicu
854	5	10.2	311	8	Q95798	Q95798 emoi impar	927	5	10.2	345	8	Q9MJT0	Q9MJT0 emys orbicu
855	5	10.2	311	8	Q95799	Q95799 emoi impar	928	5	10.2	345	8	Q9MJS9	Q9MJS9 emys orbicu
856	5	10.2	311	8	Q95800	Q95800 emoi impar	929	5	10.2	345	8	Q9MJS8	Q9MJS8 terrapene o
857	5	10.2	311	8	Q95805	Q95805 emoi pseud	930	5	10.2	345	8	Q9MJS7	Q9MJS7 clemmys ins
858	5	10.2	311	8	Q95806	Q95806 emoi pseud	931	5	10.2	345	8	Q9MJS6	Q9MJS6 clemmys gut
859	5	10.2	311	8	Q96115	Q96115 emoi caeru	932	5	10.2	345	8	Q9MJS5	Q9MJS5 clemmys mar
860	5	10.2	311	8	Q34411	Q34411 emoi caeru	933	5	10.2	345	8	Q9MJS4	Q9MJS4 clemmys muh
861	5	10.2	311	8	Q34414	Q34414 emoi caeru	934	5	10.2	345	8	Q9MJS3	Q9MJS3 emydoldea b
862	5	10.2	311	8	Q34465	Q34465 emoi impar	935	5	10.2	345	8	Q9MJS2	Q9MJS2 emys orbicu
863	5	10.2	311	8	Q34466	Q34466 emoi impar	936	5	10.2	345	8	Q9MDP0	Q9MDP0 emys orbicu
864	5	10.2	312	10	Q9MIF0	Q9MIF0 arabidopsis	937	5	10.2	345	8	Q9MDC5	Q9MDC5 emys orbicu
865	5	10.2	314	2	Q9KAC3	Q9KAC3 helicobacte	938	5	10.2	345	8	Q9MDA7	Q9MDA7 emys orbicu
866	5	10.2	315	2	Q9KAC6	Q9KAC6 bacillus ha	939	5	10.2	345	8	Q9MDA6	Q9MDA6 emys orbicu
867	5	10.2	318	10	Q23303	Q23303 arabidopsis	940	5	10.2	345	14	Q66098	Q66098 carnation r
868	5	10.2	318	10	Q9LYB2	Q9LYB2 arabidopsis	941	5	10.2	346	2	Q48391	Q48391 klebsiella
869	5	10.2	319	5	Q20054	Q20054 caenorhabdi	942	5	10.2	347	8	Q63399	Q63399 chlorochrys
870	5	10.2	319	11	Q9JKA5	Q9JKA5 mus musculu	943	5	10.2	347	8	Q63401	Q63401 chlorophoni
871	5	10.2	320	3	Q13842	Q13842 schizosacch	944	5	10.2	347	8	Q63406	Q63406 ciissopis le
872	5	10.2	320	5	Q45814	Q45814 caenorhabdi	945	5	10.2	347	8	Q63409	Q63409 creurgops d
873	5	10.2	321	8	Q99260	Q99260 damaliscus	946	5	10.2	347	8	Q63413	Q63413 delothraupi
874	5	10.2	322	5	Q21471	Q21471 caenorhabdi	947	5	10.2	347	8	Q63417	Q63417 euphonia la
875	5	10.2	323	5	Q9VWH9	Q9VWH9 drosophila	948	5	10.2	347	8	Q63422	Q63422 iridosornis
876	5	10.2	324	2	Q56699	Q56699 vibrio harv	949	5	10.2	347	8	Q63427	Q63427 neothraupis
877	5	10.2	324	8	Q79326	Q79326 capra ibex	950	5	10.2	347	8	Q63431	Q63431 pipraeidea
878	5	10.2	325	5	Q21104	Q21104 caenorhabdi	951	5	10.2	347	8	Q63438	Q63438 tangara gyr
879	5	10.2	325	5	Q33244	Q33244 caenorhabdi	952	5	10.2	347	8	Q63928	Q63928 schistochia
880	5	10.2	326	2	Q45727	Q45727 bacillus th	953	5	10.2	347	8	Q99250	Q99250 piranga rub
881	5	10.2	326	10	Q9M826	Q9M826 arabidopsis	954	5	10.2	347	8	Q21634	Q21634 lacerta med
882	5	10.2	327	10	Q9LYB2	Q9LYB2 arabidopsis	955	5	10.2	347	8	Q9TB31	Q9TB31 akapia john
883	5	10.2	329	8	Q79321	Q79321 capra ibex	956	5	10.2	347	8	Q9MM81	Q9MM81 algroides
884	5	10.2	329	8	Q79328	Q79328 capra pyren	957	5	10.2	347	8	Q9MM80	Q9MM80 lacerta mon
885	5	10.2	329	8	Q79329	Q79329 capra pyren	958	5	10.2	347	8	Q9MM79	Q9MM79 podarcis si
886	5	10.2	329	8	Q9T583	Q9T583 capra pyren	959	5	10.2	347	8	Q9MM78	Q9MM78 ophisops el
887	5	10.2	329	8	Q9T582	Q9T582 capra pyren	960	5	10.2	347	8	Q9MM77	Q9MM77 takydromus
888	5	10.2	329	8	Q9T4F5	Q9T4F5 capra pyren	961	5	10.2	347	8	Q9MM76	Q9MM76 gallotia ga
889	5	10.2	329	8	Q9T342	Q9T342 capra pyren	962	5	10.2	347	8	Q9MM75	Q9MM75 psammodromu
890	5	10.2	330	2	Q07474	Q07474 staphylococ	963	5	10.2	347	8	Q9MM74	Q9MM74 acanthodact
891	5	10.2	330	2	Q07859	Q07859 staphylococ	964	5	10.2	347	8	Q9MM73	Q9MM73 lacerta and
892	5	10.2	331	2	Q9PMD1	Q9PMD1 campylobact	965	5	10.2	347	8	Q9MM71	Q9MM71 adolfus jac
893	5	10.2	331	5	Q9T262	Q9T262 plasmodium	966	5	10.2	347	8	Q9MM70	Q9MM70 meroles sub
894	5	10.2	331	10	Q39954	Q39954 hellanthus	967	5	10.2	347	8	Q9MM69	Q9MM69 tropidosaur
895	5	10.2	332	1	Q27009	Q27009 methanobact	968	5	10.2	347	8	Q9MM66	Q9MM66 hellibolus

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969 5 10.2 347 8 Q9MM65
970 5 10.2 347 8 Q9MM64
971 5 10.2 347 10 Q82063
972 5 10.2 348 8 Q95777
973 5 10.2 348 8 Q95935
974 5 10.2 348 8 Q95962
975 5 10.2 349 1 Q74028
976 5 10.2 349 1 Q59575
977 5 10.2 349 2 P71492
978 5 10.2 349 2 Q9PCN2
979 5 10.2 350 5 Q20618
980 5 10.2 350 10 Q82279
981 5 10.2 351 10 Q9SYX6
982 5 10.2 351 10 Q9LRZ4
983 5 10.2 352 2 Q9KTZ1
984 5 10.2 352 8 Q9TFA4
985 5 10.2 352 13 Q9PSU8
986 5 10.2 352 13 Q9PSU7
987 5 10.2 353 5 Q21051
988 5 10.2 353 8 Q9TE69
989 5 10.2 353 8 Q9TE65
990 5 10.2 354 10 Q04440
991 5 10.2 355 2 Q9W009
992 5 10.2 355 8 Q9TEF8
993 5 10.2 357 4 Q9NSW6
994 5 10.2 358 2 Q9PIH3
995 5 10.2 358 4 Q75769
996 5 10.2 359 2 Q9KHV8
997 5 10.2 359 4 Q13394
998 5 10.2 359 4 Q9Y586
999 5 10.2 359 5 Q62031
1000 5 10.2 359 5 Q20880

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## ALIGNMENTS

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RESULT 1
Q9YVB3 ID Q9YVB3 PRELIMINARY; PRT; 293 AA.
AC Q9YVB3;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT)
OS Human respiratory syncytial virus
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VV6973;
RX MEDLINE=99022964; PubMed=9806017;
RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
RT "Antigenic and genetic diversity among the attachment proteins of
RT group A respiratory syncytial viruses that have caused repeat
RT infections in children.";
RL J. Infect. Dis. 178:925-932(1998).
DR EMBL; AF065407; AAD02943.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR INTERPRO; IPR002965; -
DR PFAM; PF00802; Glycoprotein G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 293 AA; 32125 MW; 17B5B43396A63CCF CRC64;

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Query Match 100.0%; Score 49; DB 14; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KORQKPPSKPNDFHFVFNFPVPCISCSNNPTCWAICKRIPNKKPGK 49
Db 144 KORQKPPSKPNDFHFVFNFPVPCISCSNNPTCWAICKRIPNKKPGK 192

RESULT 2
Q9YVB2 ID Q9YVB2 PRELIMINARY; PRT; 292 AA.
AC Q9YVB2;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT)
OS Human respiratory syncytial virus
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VV19983;
RX MEDLINE=99022964; PubMed=9806017;
RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
RT "Antigenic and genetic diversity among the attachment proteins of
RT group A respiratory syncytial viruses that have caused repeat
RT infections in children.";
RL J. Infect. Dis. 178:925-932(1998).
DR EMBL; AF065408; AAD02944.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR INTERPRO; IPR002965; -
DR PFAM; PF00802; Glycoprotein G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 292 AA; 31964 MW; 8942A8DD0A402A4B CRC64;

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Query Match 98.0%; Score 48; DB 14; Length 292;
Best Local Similarity 100.0%; Pred. No. 3.9e-45;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KORQKPPSKPNDFHFVFNFPVPCISCSNNPTCWAICKRIPNKKPGK 48
Db 144 KORQKPPSKPNDFHFVFNFPVPCISCSNNPTCWAICKRIPNKKPGK 191

RESULT 3
Q86356 ID Q86356 PRELIMINARY; PRT; 295 AA.
AC Q86356;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE G PROTEIN (FRAGMENT)
OS respiratory syncytial virus
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=12814;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RSB89-1734;
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
RT subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RSB89-1734;
RX Cane P.A.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X73350; CAA51761.1; -
DR INTERPRO; IPR000255; -

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DR INTERPRO; IPR000925; -.
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 295 AA; 32527 MW; D32BE769E0A23CFA CRC64;

Query Match 98.0%; Score 48; DB 14; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-45;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDHFVEVFNVPSCSNNPTCWAICKRIPNKKPGK 48
Db 147 KORQKPPSKPNDHFVEVFNVPSCSNNPTCWAICKRIPNKKPGK 194

RESULT 4
Q86360
ID Q86360 PRELIMINARY; PRT; 295 AA.
AC Q86360;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE G PROTEIN (FRAGMENT);
OS respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=12814;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RSB89-642;
RX MEDLINE=91374045; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RSB89-642;
RA Cane P.A.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X73354; CAA51765.1; -.
DR INTERPRO; IPR000255; -.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 295 AA; 32306 MW; 671DCF044157D284 CRC64;

Query Match 98.0%; Score 48; DB 14; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-45;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDHFVEVFNVPSCSNNPTCWAICKRIPNKKPGK 48
Db 147 KORQKPPSKPNDHFVEVFNVPSCSNNPTCWAICKRIPNKKPGK 194

RESULT 5
Q82066
ID Q82066 PRELIMINARY; PRT; 297 AA.
AC Q82066;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE GLYCOPROTEIN.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]

DR INTERPRO; IPR000925; -.
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 295 AA; 32527 MW; D32BE769E0A23CFA CRC64;

Query Match 98.0%; Score 48; DB 14; Length 297;
Best Local Similarity 100.0%; Pred. No. 4e-45;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDHFVEVFNVPSCSNNPTCWAICKRIPNKKPGK 48
Db 149 KORQKPPSKPNDHFVEVFNVPSCSNNPTCWAICKRIPNKKPGK 196

RESULT 6
Q82067
ID Q82067 PRELIMINARY; PRT; 297 AA.
AC Q82067;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE GLYCOPROTEIN.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUBGROUP A;
RX MEDLINE=94335057; PubMed=8057427;
RA Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,
Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
Melero J.A.;
RT "Evolutionary pattern of human respiratory syncytial virus (subgroup
A): cocirculating lineages and correlation of genetic and antigenic
changes in the G glycoprotein.";
RL J. Virol. 68:5448-5459(1994).
DR EMBL; Z33427; CAA83870.1; -.
DR INTERPRO; IPR000925; -.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
SQ SEQUENCE 297 AA; 32589 MW; F210F8C68193F5DD CRC64;

Query Match 98.0%; Score 48; DB 14; Length 297;
Best Local Similarity 100.0%; Pred. No. 4e-45;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDHFVEVFNVPSCSNNPTCWAICKRIPNKKPGK 48
Db 149 KORQKPPSKPNDHFVEVFNVPSCSNNPTCWAICKRIPNKKPGK 196

RESULT 7
Q82071
ID Q82071 PRELIMINARY; PRT; 297 AA.
AC Q82071;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
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DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE GLYCOPROTEIN.  
 GN G.  
 OS Human respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11250;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SUBGROUP A;  
 RX MEDLINE=94335057; PubMed=8057427;  
 RA Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,  
 RA Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,  
 RA Melero J.A.;  
 RT "Evolutionary pattern of human respiratory syncytial virus (subgroup  
 A): cocirculating lineages and correlation of genetic and antigenic  
 changes in the G glycoprotein.";  
 RL J. Virol. 68:5448-5459(1994).  
 DR EMBL; Z33432; CAA83875.1; -;  
 DR INTERPRO; IPR000255; -;  
 DR INTERPRO; IPR000925; -;  
 DR PFAM; PF00802; Glycoprotein\_G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN\_1.  
 SQ SEQUENCE 297 AA; 32581 MW; AD947B2318193306 CRC64;

Query Match 98.0%; Score 48; DB 14; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 4e-45; Indels 0; Gaps 0;  
 Matches 48; Conservative 0; Mismatches 0;

QY 1 KORONKPPSPNNDHFHFVPCSCSNNPTCWAICKRIPNKKPGK 48  
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 Db 149 KORONKPPSPNNDHFHFVPCSCSNNPTCWAICKRIPNKKPGK 196

RESULT 8  
 QYVB5 PRELIMINARY; PRT; 297 AA.  
 ID QYVB5  
 AC QYVB5  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE ATTACHMENT GLYCOPROTEIN G.  
 OS Human respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11250;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WV2780;  
 RX MEDLINE=99022964; PubMed=9806017;  
 RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;  
 RT "Antigenic and genetic diversity among the attachment proteins of  
 group A respiratory syncytial viruses that have caused repeat  
 infections in children.";  
 RL J. Infect. Dis. 178:925-932(1998).  
 DR EMBL; AF065405; AAD02941.1; -;  
 DR INTERPRO; IPR000255; -;  
 DR INTERPRO; IPR000925; -;  
 DR INTERPRO; IPR002965; -;  
 DR PFAM; PF00802; Glycoprotein\_G; 1.  
 DR PRINTS; PR01217; PRICEXTENS.  
 DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN\_1.  
 SQ SEQUENCE 297 AA; 32572 MW; 5C10E719A05EF5C1 CRC64;

Query Match 98.0%; Score 48; DB 14; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 4e-45; Indels 0; Gaps 0;  
 Matches 48; Conservative 0; Mismatches 0;

QY 1 KORONKPPSPNNDHFHFVPCSCSNNPTCWAICKRIPNKKPGK 48  
 ||||||||||||||||||||||||||||||||||||||||||||

Db 149 KORONKPPSPNNDHFHFVPCSCSNNPTCWAICKRIPNKKPGK 196

RESULT 9  
 QYVB5 PRELIMINARY; PRT; 297 AA.  
 ID QYVB5  
 AC QYVB5  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE ATTACHMENT PROTEIN.  
 GN G.  
 OS Human respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11250;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CH34;  
 RX MEDLINE=98418504; PubMed=9747732;  
 RA Peret T.C.F., Hall C.B., Schnabel K.C., Golub J.A., Anderson L.J.;  
 RT "Circulation patterns of genetically distinct group A and B strains of  
 human respiratory syncytial virus in a community.";  
 RL J. Gen. Virol. 79:2221-2229(1998).  
 DR EMBL; AF065257; AAC36327.1; -;  
 DR INTERPRO; IPR000255; -;  
 DR INTERPRO; IPR000925; -;  
 DR PFAM; PF00802; Glycoprotein\_G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN\_1.  
 SQ SEQUENCE 297 AA; 32564 MW; 377C7CBC0D0A3645 CRC64;

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QY 7 PPSKPNNDHFHFVPCSCSNNPTCWAICKRIPNKKPGK 48  
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 Db 155 PPSKPNNDHFHFVPCSCSNNPTCWAICKRIPNKKPGK 196

RESULT 10  
 QYVB5 PRELIMINARY; PRT; 297 AA.  
 ID QYVB5  
 AC QYVB5  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE GLYCOPROTEIN.  
 GN G.  
 OS Human respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11250;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SUBGROUP A;  
 RX MEDLINE=94335057; PubMed=8057427;  
 RA Garcia O., Martin M., Dopazo J., Arbiza J., Fabrasile S., Russi J.,  
 RA Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,  
 RA Melero J.A.;  
 RT "Evolutionary pattern of human respiratory syncytial virus (subgroup  
 A): cocirculating lineages and correlation of genetic and antigenic  
 changes in the G glycoprotein.";  
 RL J. Virol. 68:5448-5459(1994).  
 DR EMBL; Z33431; CAA83874.1; -;  
 DR INTERPRO; IPR000255; -;  
 DR INTERPRO; IPR000925; -;  
 DR PFAM; PF00802; Glycoprotein\_G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN\_1.  
 SQ SEQUENCE 297 AA; 32518 MW; EE913CBF1259BB8 CRC64;

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Query Match      83.7%; Score 41; DB 14; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PSKNNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPKG 48
    |||||
Db 156 PSKNNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPKG 196

RESULT 11
Q906U1 ID Q906U1 PRELIMINARY; PRT; 278 AA.
AC Q906U1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91142;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193305; AAF23728.1;
DR INTERPRO; IPR000255;
DR INTERPRO; IPR000255;
DR INTERPRO; IPR002965;
DR PRAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30461 MW; AC113DCCDF47EDE CRC64;

Query Match      81.6%; Score 40; DB 14; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KPNNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPKG 49
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Db 139 KPNNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPKG 178

RESULT 12
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AC Q906T7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92308;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193309; AAF23732.1;
DR INTERPRO; IPR000255;

Query Match      81.6%; Score 40; DB 14; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 139 KPNNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPKG 178

RESULT 13
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AC Q906T4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92528;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193312; AAF23735.1;
DR INTERPRO; IPR000255;
DR INTERPRO; IPR000925;
DR INTERPRO; IPR002965;
DR PRAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30474 MW; 2E05963863BF8A75 CRC64;

Query Match      81.6%; Score 40; DB 14; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 139 KPNNDFHFEVFNPCSCSNNPTCWAICKRIPNKKPKG 178

RESULT 14
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AC Q906T3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN-93006;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193313; AAF23736.1; -.
DR INTERPRO; IPR000255; -.
DR INTERPRO; IPR000925; -.
DR INTERPRO; IPR002965; -.
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30443 MW; 8E2974F2E1AE15C9 CRC64;

Query Match      81.6%; Score 40; DB 14; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDFHEVFNFVPCISCSNNPTCWAICKRIPNKKPGKK 49
Db 139 KPNDFHEVFNFVPCISCSNNPTCWAICKRIPNKKPGKK 178
|||||
RESULT 15
Q906T1 PRELIMINARY; PRT; 278 AA.
AC Q906T1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-94118;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193315; AAF23738.1; -.
DR INTERPRO; IPR000255; -.
DR INTERPRO; IPR000925; -.
DR INTERPRO; IPR002965; -.
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30481 MW; 86F307049A641648 CRC64;

Query Match      81.6%; Score 40; DB 14; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.3e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNDFHEVFNFVPCISCSNNPTCWAICKRIPNKKPGKK 49
Db 139 KPNDFHEVFNFVPCISCSNNPTCWAICKRIPNKKPGKK 178
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Search completed: May 21, 2001, 14:19:31  
Job time: 99 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 21, 2001, 14:14:51 ; Search time 18.63 Seconds  
(without alignments)  
150.349 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	288	100.0	49	19	Human RSV A subtyp
2	288	100.0	49	19	Human RSV G protei
3	288	100.0	49	19	Human RSV G protei
4	288	100.0	49	19	Human RSV G protei
5	288	100.0	49	19	Human RSV G protei
6	288	100.0	298	8	Sequence of human
7	288	100.0	298	13	HSRV glycoprotein
8	288	100.0	298	19	HSRV glycoprotein
9	288	100.0	681	10	Chimeric human res
10	285	99.0	49	19	Human RSV A subtyp
11	285	99.0	49	19	Human RSV A subtyp

12	285	99.0	49	19	W39221	Human RSV A subtyp
13	285	99.0	49	19	W39222	Human RSV A subtyp
14	285	99.0	49	19	W39223	Human RSV A subtyp
15	285	99.0	49	19	W39224	Human RSV A subtyp
16	285	99.0	59	17	R97073	Respiratory Syncyt
17	285	99.0	59	20	Y44100	RSV G protein anti
18	285	99.0	61	17	R97072	Respiratory Syncyt
19	285	99.0	61	20	Y44099	RSV G protein anti
20	285	99.0	101	16	R88253	RSV sub-group A wi
21	285	99.0	101	17	R95610	RSV sub-group A wi
22	285	99.0	101	17	R95616	Respiratory Syncyt
23	285	99.0	101	17	R97050	Respiratory Syncyt
24	285	99.0	101	20	Y44078	RSV G protein anti
25	285	99.0	101	21	B18805	A G2Na peptide der
26	285	99.0	232	20	W96314	Secreted G protein
27	285	99.0	298	14	R39286	Respiratory syncyt
28	285	99.0	298	20	W96313	Membrane bound G p
29	285	99.0	349	17	R95660	Streptococcal prot
30	283	98.3	49	19	W39220	Human RSV A subtyp
31	280	97.2	57	17	R97074	Respiratory Syncyt
32	280	97.2	57	20	Y44101	RSV G protein anti
33	270	93.8	101	20	W97311	Peptide which indu
34	269	93.4	55	17	R97075	Respiratory Syncyt
35	269	93.4	55	20	Y44102	RSV G protein anti
36	267	92.7	101	20	W97310	Peptide which indu
37	265	92.0	59	17	R97080	Respiratory Syncyt
38	265	92.0	59	20	Y44107	RSV G protein anti
39	265	92.0	61	17	R97079	Respiratory Syncyt
40	265	92.0	61	20	Y44106	RSV G protein anti
41	265	92.0	101	16	R88255	RSV sub-group A mod
42	265	92.0	101	17	R95612	RSV sub-group A mu
43	265	92.0	101	17	R95618	Respiratory Syncyt
44	265	92.0	101	17	R97052	Respiratory Syncyt
45	265	92.0	101	20	Y44080	RSV G protein anti

#### ALIGNMENTS

RESULT 1  
W39217  
ID W39217 standard; peptide; 49 AA.  
XX  
XX W39217;  
XX AC  
XX  
XX  
XX 27-AUG-1998 (first entry)  
XX Human RSV A subtype G protein fragment (aa. 149-157) strain A2.  
XX  
XX  
XX G protein; treatment; prevention; diagnosis; infection; immunity;  
XX antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX  
XX Human respiratory syncytial virus.  
XX  
XX Key Location/Qualifiers  
XX Disulfide-bond 25...38  
XX Disulfide-bond 28...34  
XX  
XX W09746581-A1.  
XX  
XX 11-DEC-1997.  
XX  
XX 04-JUN-1997; 97WO-AU00351.  
XX  
XX 05-JUN-1996; 96AU-0000265.  
XX  
XX (BIOM-) BIOMOLECULAR RES INST LTD.  
XX  
XX Gorman JJ;  
XX  
XX WPI; 1998-042117/04.  
XX  
XX Peptide(s) derived from specific region of respiratory syncytial

PT virus G protein - used to treat, prevent, diagnose and immunise  
PT against Pneumovirus infection  
XX  
XX  
PS Claim 5; Fig 2; 75pp; English.  
XX  
CC W39217-W39234 are fragments of the human respiratory syncytial virus  
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to host  
CC cells and for characterisation of cell receptors for Pneumoviruses. When  
CC the fragments are used in combination with existing vaccines, they may  
CC allow a reduction in dose, and thus side effects, of the vaccine.  
XX  
XX Sequence 49 AA;  
SQ

Query Match 100.0%; Score 288; DB 19; Length 49;  
Best Local Similarity 100.0%; Pred. No. 9.2e-29;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDHFVFVPCISCSNPTCWAICKRIPNKKPGKK 49  
|||||  
DB 1 kqrqkppskpndhfefvfpvcsicsnptcwaickripnkkpgkk 49  
|||||

RESULT 2  
W39244  
ID W39244 standard; peptide; 49 AA.  
XX AC W39244;  
XX  
XX 27-AUG-1998 (first entry)  
XX  
DE Human RSV G protein fragment (aa. 149-157) derivative #1.  
XX  
XX G protein; treatment; prevention; diagnosis; infection; immunity;  
KW antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX  
XX Human respiratory syncytial virus.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal acetylated"  
FT Disulfide-bond 25..38  
FT Disulfide-bond 28..34  
FT Modified-site 49  
FT /note= "C-terminal amide"  
XX  
XX WO9746581-A1.  
XX  
XX 11-DEC-1997.  
XX  
XX 04-JUN-1997; 97WO-AU00351.  
XX  
XX 05-JUN-1996; 96AU-0000265.  
XX  
XX (BIOM-) BIOMOLECULAR RES INST LTD.  
XX  
XX Gorman JJ;  
XX  
XX WPI; 1998-042117/04.  
XX  
XX Peptide(s) derived from specific region of respiratory syncytial  
PT virus G protein - used to treat, prevent, diagnose and immunise  
PT against Pneumovirus infection  
XX  
XX Example 4; Fig 12; 75pp; English.  
XX  
XX W39244-W39252 are derivatives of the human respiratory syncytial virus  
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to host  
CC cells and for characterisation of cell receptors for Pneumoviruses. When  
CC the fragments are used in combination with existing vaccines, they may  
CC allow a reduction in dose, and thus side effects, of the vaccine.  
XX  
XX Sequence 49 AA;  
SQ

Query Match 100.0%; Score 288; DB 19; Length 49;  
Best Local Similarity 100.0%; Pred. No. 9.2e-29;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDHFVFVPCISCSNPTCWAICKRIPNKKPGKK 49  
|||||  
DB 1 kqrqkppskpndhfefvfpvcsicsnptcwaickripnkkpgkk 49  
|||||

RESULT 3  
W39248  
ID W39248 standard; peptide; 49 AA.  
XX AC W39248;  
XX  
XX 27-AUG-1998 (first entry)  
XX  
DE Human RSV G protein fragment (aa. 149-157) derivative #5.  
XX  
XX G protein; treatment; prevention; diagnosis; infection; immunity;  
KW antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX  
XX Human respiratory syncytial virus.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal fitc group"  
FT Disulfide-bond 25..38  
FT Disulfide-bond 28..34  
FT Modified-site 49  
FT /note= "C-terminal amide"  
XX  
XX WO9746581-A1.  
XX  
XX 11-DEC-1997.  
XX  
XX 04-JUN-1997; 97WO-AU00351.  
XX  
XX 05-JUN-1996; 96AU-0000265.  
XX  
XX (BIOM-) BIOMOLECULAR RES INST LTD.  
XX  
XX Gorman JJ;  
XX  
XX WPI; 1998-042117/04.  
XX  
XX Peptide(s) derived from specific region of respiratory syncytial  
PT virus G protein - used to treat, prevent, diagnose and immunise  
PT against Pneumovirus infection  
XX  
XX Example 4; Fig 12; 75pp; English.  
XX  
XX W39244-W39252 are derivatives of the human respiratory syncytial virus  
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to host  
CC cells and for characterisation of cell receptors for Pneumoviruses. When  
CC the fragments are used in combination with existing vaccines, they may  
CC allow a reduction in dose, and thus side effects, of the vaccine.  
XX  
XX Sequence 49 AA;  
SQ

Db 1 kqrqkppskpndfhfevfpcscsnnptcwaickripnkpgkk 49

Query Match 100.0%; Score 288; DB 19; Length 49;  
Best Local Similarity 100.0%; Pred. No. 9.2e-29;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNDHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 49  
|||||  
Db 1 kqrqkppskpndfhfevfpcscsnnptcwaickripnkpgkk 49

RESULT 4  
W39250  
ID W39250 standard; peptide; 49 AA.  
XX AC W39250;  
XX DT 27-AUG-1998 (first entry)  
XX DE Human RSV G protein fragment (aa. 149-157) derivative #7.  
XX KW G protein; treatment; prevention; diagnosis; infection; immunity;  
XX KW antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX OS Human respiratory syncytial virus.  
XX FH Key Location/Qualifiers  
XX FT Modified-site 1 /note= "N-terminal bb group"  
XX FT Disulfide-bond 25..38  
XX FT Disulfide-bond 28..34  
XX FT Modified-site 49  
XX FT /note= "C-terminal amide"  
XX PN WO9746581-A1.  
XX PD 11-DEC-1997.  
XX PF 04-JUN-1997; 97WO-AU00351.  
XX PR 05-JUN-1996; 96AU-0000265.  
XX PA (BIOM-) BIOMOLECULAR RES INST LTD.  
XX PI Gorman JJ;  
XX DR WPI; 1998-042117/04.  
XX PT Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection  
XX PS Example 4; Fig 12; 75pp; English.  
XX CC W39244-W39252 are derivatives of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to identify compounds able to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.

Sequence 49 AA;

Query Match 100.0%; Score 288; DB 19; Length 49;  
Best Local Similarity 100.0%; Pred. No. 9.2e-29;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNDHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 49  
|||||

RESULT 5  
W39251  
ID W39251 standard; peptide; 49 AA.  
XX AC W39251;  
XX DT 27-AUG-1998 (first entry)  
XX DE Human RSV G protein fragment (aa. 149-157) derivative #8.  
XX KW G protein; treatment; prevention; diagnosis; infection; immunity;  
XX KW antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX OS Human respiratory syncytial virus.  
XX FH Key Location/Qualifiers  
XX FT Modified-site 1 /note= "N-terminal blot group"  
XX FT Disulfide-bond 25..38  
XX FT Disulfide-bond 28..34  
XX FT Modified-site 49  
XX FT /note= "C-terminal amide"  
XX PN WO9746581-A1.  
XX PD 11-DEC-1997.  
XX PF 04-JUN-1997; 97WO-AU00351.  
XX PR 05-JUN-1996; 96AU-0000265.  
XX PA (BIOM-) BIOMOLECULAR RES INST LTD.  
XX PI Gorman JJ;  
XX DR WPI; 1998-042117/04.  
XX PT Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection  
XX PS Example 4; Fig 12; 75pp; English.  
XX CC W39244-W39252 are derivatives of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to identify compounds able to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.

Sequence 49 AA;

Query Match 100.0%; Score 288; DB 19; Length 49;  
Best Local Similarity 100.0%; Pred. No. 9.2e-29;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNDHFVFNPCSCSNNPTCWAICKRIPNKKPGKK 49  
|||||  
Db 1 kqrqkppskpndfhfevfpcscsnnptcwaickripnkpgkk 49

RESULT 6

ID P70845 standard; protein; 298 AA.  
XX AC P70845;

XX 05-APR-1991 (first entry)  
 XX Sequence of human respiratory syncytial virus (HRSV) A2 strain  
 DE G protein.  
 DE XX  
 KW Vaccine.  
 XX  
 OS Human respiratory syncytial virus (HRSV).  
 XX  
 PN W08704185-A.  
 XX  
 PD 16-JUL-1987.  
 XX  
 XX 23-DEC-1986; 86WO-US02756.  
 PF  
 XX 14-JAN-1986; 86US-0818740.  
 PR  
 XX (UYNC-) UNIV OF N CAROLINA.  
 PA (WERTZ) WERTZ G W.  
 PA (WERTZ) WERTZ G W.  
 XX  
 XX WPI: 1987-206300/29.  
 DR N-PSDB; N70784.  
 XX  
 XX Vaccines for human respiratory virus - comprising proteins or  
 PT fragment encoded by a DNA sequence coding for human respiratory  
 PT syncytial virus proteins.  
 XX  
 PS Disclosure; Chart 13; 57pp; English.  
 XX  
 CC A novel plasmid which comprises a DNA sequence encoding this  
 CC protein, and the protein itself, are claimed, for use as HRSV  
 CC vaccines. The vaccine can be administered to pregnant women or to  
 CC women of child bearing age to stimulate maternal antibodies.  
 CC Infants can also be vaccinated at 2-3 months of age.  
 XX  
 SQ Sequence 298 AA;

Query Match 100.0%; Score 288; DB 8; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-28;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDDHFEVFNVPSCISCSNPTCWAICKRIPNKKPGKK 49  
 |||||  
 Db 149 kqrqkppskpndhfevfnvpsciscsnptcwaickripnkkpgkk 197

RESULT 7  
 R25302  
 ID R25302 standard; Protein; 298 AA.  
 XX  
 AC R25302;  
 XX  
 XX 03-MAR-1993 (first entry)  
 DT  
 XX HRSV glycoprotein G (gpG).  
 DE  
 XX Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K;  
 KW major capsid protein; N.  
 KW  
 XX Human respiratory syncytial virus strain A2.  
 OS  
 XX US5149650-A.  
 PN  
 XX 22-SEP-1992.  
 PD  
 XX 14-JAN-1986; 86US-0818740.  
 PF  
 XX 14-JAN-1986; 86US-0818740.  
 PR  
 XX 13-JUL-1988; 88US-0218737.  
 XX

PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Collins PL, Wertz GW;  
 XX  
 DR WPI: 1992-340247/41.  
 DR N-PSDB; Q29623.  
 XX  
 XX Vaccines for human respiratory virus - include structural genes  
 PT coding for native structural viral proteins and immunogenic  
 PT fragments  
 XX  
 XX Disclosure; Page 18; 21pp; English.  
 PS  
 XX The sequences of mRNA encoding HRSV structural proteins are given in  
 CC Q29622-26. The proteins are F, G, 22K, 9.5K and major capsid  
 CC protein N. The sequences and encoded proteins are useful for  
 CC preparing vaccines against HRSV. The vaccines can be used to confer  
 CC immunity against respiratory tract infections on human subjects.  
 XX  
 SQ Sequence 298 AA;

Query Match 100.0%; Score 288; DB 13; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-28;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDDHFEVFNVPSCISCSNPTCWAICKRIPNKKPGKK 49  
 |||||  
 Db 149 kqrqkppskpndhfevfnvpsciscsnptcwaickripnkkpgkk 197

RESULT 8  
 W47605  
 ID W47605 standard; Protein; 298 AA.  
 XX  
 AC W47605;  
 XX  
 XX 11-JUN-1998 (first entry)  
 DT  
 XX HRSV glycoprotein G.  
 DE  
 XX HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine.  
 KW  
 XX Human respiratory syncytial virus.  
 OS  
 XX US5716823-A.  
 PN  
 XX 10-FEB-1998.  
 PD  
 XX 12-MAY-1997; 97US-0854783.  
 PF  
 XX 13-JUL-1988; 88US-0218737.  
 PR  
 XX 14-JAN-1986; 86US-0818740.  
 PR  
 XX 23-DEC-1986; 86WO-US02756.  
 PR  
 XX 11-JUN-1992; 92US-0897171.  
 PR  
 XX 12-MAY-1997; 97US-0854783.  
 XX  
 XX (PHAA ) PHARMACIA & UPJOHN CO.  
 PA  
 XX Collins PL, Wertz GW;  
 PI  
 XX WPI: 1998-144802/13.  
 DR  
 XX N-PSDB; V18736.  
 DR  
 XX Production of human respiratory syncytial virus glyco-protein F or G  
 PT - by culturing eukaryotic host cells transfected with corresponding  
 PT DNA  
 XX  
 XX Example 1; Columns 27-28; 17pp; English.  
 PS  
 XX The present sequence was used in the development of a novel method  
 CC for the production of human respiratory syncytial virus (HRSV)  
 CC glycoprotein F (gpF) or glycoprotein G (gpG). The method comprises

XX

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
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91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

XX	Gorman JJ;
PI	WPI; 1998-042117/04.
DR	Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection
PT	Claim 5; Fig 2; 75pp; English.
PS	W39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to identify compounds able to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
SS	Sequence 49 AA;
SQ	
Query Match	99.0%; Score 285; DB 19; Length 49;
Best Local Similarity	98.0%; Pred. No. 2.2e-28;
Matches 48; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KQRNQPPKPNNDFFHFVFNFPCISCSNNPTCWAICKRIPNKKPGKK 49      :     :     :     :     :     :     :     :
Dd	1 kqrqnpkpnndfhfvfnfpciscsnptcwaickripnkpgkk 49
RESULT 13	
W39222	ID W39222 standard; peptide; 49 AA.
AC	W39222;
DT	27-AUG-1998 (first entry)
XX	Human RSV A subtype G protein fragment (aa. 149-157) strain A6190.
DE	G protein; treatment; prevention; diagnosis; infection; immunity; antibody; Pneumovirus; identification; vaccine; cell receptor.
KW	Human respiratory syncytial virus.
OS	Key Location/Qualifiers
FH	Disulfide-bond 25..38
FT	Disulfide-bond 28..34
XX	WO9746581-A1.
PD	11-DEC-1997.
PF	04-JUN-1997; 97WO-AU00351.
PR	05-JUN-1996; 96AU-0000265.
PA	(BIOM-) BIOMOLECULAR RES INST LTD.
PI	Gorman JJ;
PI	WPI; 1998-042117/04.
DR	Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection
PT	Claim 5; Fig 2; 75pp; English.
PS	W39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to identify compounds able to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
SS	Sequence 49 AA;
SQ	
Query Match	99.0%; Score 285; DB 19; Length 49;
Best Local Similarity	98.0%; Pred. No. 2.2e-28;
Matches 48; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KQRNQPPKPNNDFFHFVFNFPCISCSNNPTCWAICKRIPNKKPGKK 49      :     :     :     :     :     :     :     :
Dd	1 kqrqnpkpnndfhfvfnfpciscsnptcwaickripnkpgkr 49
RESULT 12	
W39221	ID W39221 standard; peptide; 49 AA.
AC	W39221;
DT	27-AUG-1998 (first entry)
XX	Human RSV A subtype G protein fragment (aa. 149-157) strain A6256.
DE	G protein; treatment; prevention; diagnosis; infection; immunity; antibody; Pneumovirus; identification; vaccine; cell receptor.
KW	Human respiratory syncytial virus.
OS	Key Location/Qualifiers
FH	Disulfide-bond 25..38
FT	Disulfide-bond 28..34
XX	WO9746581-A1.
PD	11-DEC-1997.
PF	04-JUN-1997; 97WO-AU00351.
PR	05-JUN-1996; 96AU-0000265.
PA	(BIOM-) BIOMOLECULAR RES INST LTD.

CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to host  
CC cells and for characterisation of cell receptors for Pneumoviruses. When  
CC the fragments are used in combination with existing vaccines, they may  
CC allow a reduction in dose, and thus side effects, of the vaccine.  
XX  
SQ Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;  
Best Local Similarity 98.0%; Pred. No. 2.2e-28;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPSKPNDHFVEVFNFPVCSICSNPTCWAICKRIPNKKPGKK 49  
Db 1 kqrqnpknppndhfvevfnfvpvcsicsnnptcwaickripnkkpgkk 49

RESULT 14  
W39223  
ID W39223 standard; peptide; 49 AA.  
XX  
AC W39223;  
XX  
DT 27-AUG-1998 (first entry)  
XX  
DE Human RSV A subtype G protein fragment (aa. 149-157) strain A5857.  
XX  
KW G protein; treatment; prevention; diagnosis; infection; immunity;  
XX antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX  
OS Human respiratory syncytial virus.  
XX

FH Key Location/Qualifiers  
FT Disulfide-bond 25..38  
FT Disulfide-bond 28..34  
XX  
XX WO9746581-A1.

XX 11-DEC-1997.  
XX  
XX 04-JUN-1997; 97WO-AU00351.  
XX  
XX 05-JUN-1996; 96AU-0000265.  
XX

XX (BIOM-) BIOMOLECULAR RES INST LTD.  
XX  
XX Gorman JJ;  
XX

XX WPI; 1998-042117/04.

XX Peptide(s) derived from specific region of respiratory syncytial  
PT virus G protein - used to treat, prevent, diagnose and immunise  
PT against Pneumovirus infection  
XX

XX Claim 5; Fig 2; 75pp; English.

XX W39217-W39234 are fragments of the human respiratory syncytial virus  
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to host  
CC cells and for characterisation of cell receptors for Pneumoviruses. When  
CC the fragments are used in combination with existing vaccines, they may  
CC allow a reduction in dose, and thus side effects, of the vaccine.  
XX

XX Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;  
Best Local Similarity 98.0%; Pred. No. 2.2e-28;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPSKPNDHFVEVFNFPVCSICSNPTCWAICKRIPNKKPGKK 49  
Db 1 kqrqnpknppndhfvevfnfvpvcsicsnnptcwaickripnkkpgkk 49

RESULT 15  
W39224  
ID W39224 standard; peptide; 49 AA.  
XX  
AC W39224;  
XX

DT 27-AUG-1998 (first entry)

XX Human RSV A subtype G protein fragment (aa. 149-157) strain A1734.  
XX  
KW G protein; treatment; prevention; diagnosis; infection; immunity;  
XX antibody; Pneumovirus; identification; vaccine; cell receptor.  
XX

OS Human respiratory syncytial virus.

XX Key Location/Qualifiers  
FH Disulfide-bond 25..38  
FT Disulfide-bond 28..34  
XX

XX WO9746581-A1.

XX 11-DEC-1997.

XX 04-JUN-1997; 97WO-AU00351.

XX 05-JUN-1996; 96AU-0000265.

XX (BIOM-) BIOMOLECULAR RES INST LTD.

XX Gorman JJ;

XX WPI; 1998-042117/04.

XX Peptide(s) derived from specific region of respiratory syncytial  
PT virus G protein - used to treat, prevent, diagnose and immunise  
PT against Pneumovirus infection  
XX

XX Claim 5; Fig 2; 75pp; English.

XX W39217-W39234 are fragments of the human respiratory syncytial virus  
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments  
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,  
CC infection and to immunise against such infections. Antibodies raised  
CC from these fragments may also be used diagnostically. The fragments may  
CC also be used to identify compounds able to inhibit binding of RSV to host  
CC cells and for characterisation of cell receptors for Pneumoviruses. When  
CC the fragments are used in combination with existing vaccines, they may  
CC allow a reduction in dose, and thus side effects, of the vaccine.  
XX

XX Sequence 49 AA;

Query Match 99.0%; Score 285; DB 19; Length 49;  
Best Local Similarity 98.0%; Pred. No. 2.2e-28;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPSKPNDHFVEVFNFPVCSICSNPTCWAICKRIPNKKPGKK 49  
Db 1 kqrqnpknppndhfvevfnfvpvcsicsnnptcwaickripnkkpgkr 49

Search completed: May 21, 2001, 14:15:16  
Job time: 25 sec



Result No.	Score	Query Match	ID	Description
1	288	100.0	681	6 5194595-19 Patent No. 5194595
2	285	99.0	298	2 US-08-467-963C-8 Sequence 8, Appli
3	285	99.0	298	2 US-08-838-189D-8 Sequence 8, Appli
4	285	99.0	298	3 US-08-852-344D-8 Sequence 8, Appli
5	285	99.0	298	3 US-08-344-639E-8 Sequence 8, Appli
6	285	99.0	298	4 US-08-467-969A-8 Sequence 8, Appli
7	285	99.0	298	4 US-08-467-961A-8 Sequence 8, Appli
8	217	75.3	37	3 US-08-793-792-12 Sequence 12, Appl
9	193	67.0	32	3 US-08-793-792-8 Sequence 8, Appli
10	174	60.4	28	3 US-08-793-792-4-1 Sequence 4, Appli
11	151	52.4	37	3 US-08-793-792-11 Sequence 11, Appl
12	145	50.3	30	4 US-08-838-504A-6 Sequence 6, Appli
13	138	47.9	32	3 US-08-793-792-7 Sequence 7, Appli
14	129	44.8	30	4 US-08-836-504A-5 Sequence 5, Appli
15	125	43.4	28	3 US-08-793-792-3 Sequence 3, Appli
16	96	33.3	16	3 US-08-793-792-13 Sequence 13, Appl
17	80	27.8	263	5 PCT-US91-08177-13 Sequence 13, Appl
18	66	22.9	32	3 US-08-793-792-6 Sequence 6, Appli
19	66	22.9	37	3 US-08-793-792-10 Sequence 10, Appl
20	65	22.6	28	3 US-08-793-792-2 Sequence 2, Appli
21	64	22.2	14	4 US-08-721-979A-9 Sequence 9, Appli
22	64	22.2	14	4 US-08-836-501-9 Sequence 9, Appli
23	64	22.2	17	4 US-08-721-979A-20 Sequence 20, Appl
24	64	22.2	17	4 US-08-836-501-20 Sequence 20, Appl
25	64	22.2	28	3 US-08-793-792-1 Sequence 1, Appli
26	64	22.2	32	3 US-08-793-792-5 Sequence 5, Appli
27	64	22.2	37	3 US-08-793-792-9 Sequence 9, Appli



QY 1 KQRQKPPKPNNDFFHEVNFVPCISNNPTCWAICKRIPNKKPGKK 49  
 |||||:|||||  
 Db 149 KORQKPPKPNNDFFHEVNFVPCISNNPTCWAICKRIPNKKPGKK 197

```

RESULT 7
US-08-467-961A-8
; Sequence 8, Application US/08467961A
; Patent No. 6171783
; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasysbyn, Mary E
; TITLE OF INVENTION: Chimeric Immunogens
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Sim & McBurney  
STREET: 330 University Avenue, 6TH Floor  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,961A  
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/001,554  
FILING DATE: 06-JAN-1993

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9200117.1  
FILING DATE: 06-JAN-1992

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-476 MIS:bh  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163

TELEX: 065-24567 SIMBAS  
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
US-08-467-961A-8

Query Match 99.0%; Score 285; DB 4; Length 298;  
Best Local Similarity 98.0%; Pred. No. 1.3e-26;  
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPKNNDFEVEFVPCSCSNNPTCWAICKRIPKPKGK 49  
|||||  
DB 149 KORONKPPKNNDFEVEFVPCSCSNNPTCWAICKRIPKPKGK 197

RESULT 8

US-08-793-792-12  
Sequence 12 Application US/08793792

Patent No. 6077511  
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Antigenic peptides derived from the

TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis

TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.

NUMBER OF SEQUENCES: 13

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,792

FILING DATE:

CLASSIFICATION: 514

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-793-792-12

Query Match 75.3%; Score 217; DB 3; Length 37;  
Best Local Similarity 97.3%; Pred. No. 1.8e-19;  
Matches 36; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 SKPNDFEVEFVPCSCSNNPTCWAICKRIPKPK 45  
|||||  
DB 1 NKPNNDFEVEFVPCSCSNNPTCWAICKRIPKPK 37

RESULT 9

US-08-793-792-8  
Sequence 8 Application US/08793792

Patent No. 6077511  
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Antigenic peptides derived from the

TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis

TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.

NUMBER OF SEQUENCES: 13

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,792

FILING DATE:

CLASSIFICATION: 514

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

US-08-793-792-8

Query Match 67.0%; Score 193; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNNDFEVEFVPCSCSNNPTCWAICKRI 41  
|||||

DB 1 KPNNDFEVEFVPCSCSNNPTCWAICKRI 32

RESULT 10

US-08-793-792-4  
Sequence 4 Application US/08793792

Patent No. 6077511  
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Antigenic peptides derived from the

TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis

TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.

NUMBER OF SEQUENCES: 13

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,792

FILING DATE:

# 12-8, 4

CLASSIFICATION: 514  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-793-792-4

Query Match 60.4% Score 174 DB 3 Length 28  
Best Local Similarity 100.0% Pred. No. 1.6e-14  
Matches 28 Conservative 0 Mismatches 0 Indels 0 Gaps 0  
QY 11 PNNDFHEVFVPCISCSNPTCWAIC 38  
DB 1 PNNDFHEVFVPCISCSNPTCWAIC 28

RESULT 11  
US-08-793-792-11  
Sequence 11, Application US/08793792  
Patent No. 6077511  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Antigenic peptides derived from the  
TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis  
TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.  
NUMBER OF SEQUENCES: 13  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
APPLICATION NUMBER: US/08793792  
FILING DATE:  
CLASSIFICATION: 514  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-793-792-11

Query Match 52.4% Score 151 DB 3 Length 37;  
Best Local Similarity 69.4% Pred. No. 1.1e-11;  
Matches 25; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
QY 10 KPNDFHEVFVPCISCSNPTCWAICKRIPNKK 45  
DB 2 KPKDDYHEVFVPCISCSNPTCWAICKRIPNKK 37

RESULT 12  
US-08-836-504A-6  
Sequence 6, Application US/08836504A  
Patent No. 6130091  
GENERAL INFORMATION:  
APPLICANT: Binz, Hans  
APPLICANT: Nguyen Ngoc, Thien  
APPLICANT: Stahl, Stefan  
APPLICANT: Uhlen, Mathias  
APPLICANT: Nygren, Per Ake  
TITLE OF INVENTION: Method for obtaining a peptide derived  
TITLE OF INVENTION: from the respiratory syncytial virus, polypeptide and  
TITLE OF INVENTION: bacteria expressing it, and their applications as

TITLE OF INVENTION: medicinal product.  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rocky, Milnamow & Katz  
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,504A  
FILING DATE: 07-MAY-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Katz, Martin L.  
REGISTRATION NUMBER: 25,011  
REFERENCE/DOCKET NUMBER: PIE1514P02000S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-836-504A-6

Query Match 50.3% Score 145; DB 4; Length 30;  
Best Local Similarity 89.7% Pred. No. 4.8e-11;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 21 NVPVCSISNNPTCWAICKRIPNKKPGKK 49  
DB 1 NNPVCSISNNPTCWAICKRIPNKKPGKK 29

RESULT 13  
US-08-793-792-7  
Sequence 7, Application US/08793792  
Patent No. 6077511  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Antigenic peptides derived from the  
TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis  
TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.  
NUMBER OF SEQUENCES: 13  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
APPLICATION NUMBER: US/08793792  
FILING DATE:  
CLASSIFICATION: 514  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-793-792-7





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 21, 2001, 14:14:51 ; Search time 12.88 seconds  
(without alignments)  
261.446 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KORQNKPPSKPNDFHFEVFN.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_67:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	288	100.0	298	1 MGZ	major surface glyco
2	285	99.0	297	2 JQ1205	attachment protein
3	285	99.0	297	2 JQ1204	attachment protein
4	285	99.0	297	2 JQ1208	attachment protein
5	285	99.0	298	1 MGNZRL	major surface glyco
6	285	99.0	298	2 JC5680	G protein - Human
7	280	97.2	298	2 JQ1207	attachment protein
8	279	96.9	297	2 JQ1206	attachment protein
9	273	94.8	297	2 JQ1209	attachment protein
10	190	66.0	292	1 MGNZ18	major surface glyco
11	190	66.0	292	1 MGNZ60	major surface glyco
12	83.5	29.0	257	1 MGNZBR	major surface glyco
13	80	27.8	263	2 JQ2284	glycoprotein G - b
14	79	27.4	250	2 PQ0768	glycoprotein G - b
15	77.5	26.9	248	2 PQ0769	glycoprotein G - b
16	77.5	26.9	263	2 JQ2388	glycoprotein G - o
17	77.5	26.9	263	2 A48732	attachment glycopr
18	66.5	23.1	275	1 S01913	diaminopimelate ep
19	64	22.2	37	2 B60963	charybotoxin 2 -
20	63.5	22.0	274	2 F64090	diaminopimelate ep
21	63	21.9	1861	2 T13845	microtubule-associ
22	62	21.5	37	2 A03963	charybotoxin 1 [v
23	62	21.5	290	2 G82360	diaminopimelate ep
24	59	20.5	57	2 S70473	neurotoxin Ts-kapp
25	58.5	20.3	276	2 G82986	diaminopimelate ep
26	57.5	20.0	276	2 T10459	diaminopimelate ep
27	57.5	20.0	518	2 T25507	hypothetical prote
28	57.5	20.0	776	2 T02584	hypothetical prote
29	57	19.8	279	2 C70458	diaminopimelate ep

hypothetical prote  
gene e1 protein -  
hypothetical prote  
basic juvenile hor  
r-cell surface gly  
sex-specific stora  
hypothetical prote  
SYG1 protein - yea  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote

#### ALIGNMENTS

RESULT 1

MGZ

major surface glycoprotein G - human respiratory syncytial virus

C;Species: human respiratory syncytial virus

C;Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 24-Sep-1999

C;Accession: A94048; A93599; A04039

R;Wertz, G.W.; Collins, P.L.; Huang, Y.; Gruber, C.; Levine, S.; Ball, L.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985

A;Title: Nucleotide sequence of the G protein gene of human respiratory syncytial vir

A;Reference number: A94048; MUID:85216636

A;Accession: A94048

A;Molecule type: mRNA

A;Residues: 1-298 <WER>

A;Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217;

7.1; PID:g333932

A;Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid prot

R;State: this protein may carry 40-80 separate O-linked carbohydrate chains distribute

Nucleic Acids Res. 13, 7795-7812, 1985

A;Title: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure.

A;Reference number: A93599; MUID:86067198

A;Accession: A93599

A;Molecule type: mRNA

A;Residues: 1-298 <SAT>

A;Cross-references: GB:X03149; NID:g60997; PIDN:CAA26928.1; PID:g60998

C;Superfamily: respiratory syncytial virus major surface glycoprotein G

C;Keywords: glycoprotein; transmembrane protein

F;38-66/Domain: transmembrane #status predicted <TNM>

F;85,135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 288; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.4e-26;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPPSKPNDFHFEVFNFCISCSNNPTCWAICKRIPNKKPGKK 49

Db 149 KORQNKPPSKPNDFHFEVFNFCISCSNNPTCWAICKRIPNKKPGKK 197

RESULT 2

JQ1205

attachment protein - human respiratory syncytial virus (strain RSB1734)

N;Alternate names: G protein

C;Species: human respiratory syncytial virus

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Feb-1987

C;Accession: JQ1205

R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.

J. Gen. Virol. 72, 2091-2096, 1991

A;Title: Identification of variable domains of the attachment (G) protein of subgroup

A;Reference number: JQ1204; MUID:91374005

A;Accession: JQ1205



C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract  
er children and adults.

C;Superfamily: respiratory syncytial virus major surface glycoprotein G

C;Keywords: glycoprotein; transmembrane protein

F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) #status pred

Query Match 94.8%; Score 273; DB 2; Length 297;  
Best Local Similarity 93.9%; Pred. No. 8.1e-25;  
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDHFEEVFNVPSCISNNPTCWAICKRIPNKKPGKK 49  
|| |||||:||| ||||||||||||||||||||||||||||||||  
Db 149 KQHQNKPKNRPNHFEVEFNVPSCISNNPTCWAICKRIPNKKPGKK 197

RESULT 10

MGN218

major surface glycoprotein G - human respiratory syncytial virus (strain 18537)

C;Species: human respiratory syncytial virus

C;Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 16-Jul-1999

C;Accession: B32703

R;Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987

A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and

A;Reference number: A32703; PMID:87289657

A;Accession: B32703

A:Molecule type: mRNA

A:Residues: 1-292 <JOB>

A:CROSS-references: GB:M17213; NID:g333942; PIDN:AAA47412.1; PID:g333943

C;Superfamily: respiratory syncytial virus major surface glycoprotein G

C;Keywords: glycoprotein; transmembrane protein

F:41-63/Domain: transmembrane #status predicted <TMN>

F:81,86,100/Binding site: carbohydrate (Asn) #status predicted

Query Match 56.0%; Score 190; DB 1; Length 292;  
Best Local Similarity 55.3%; Pred. No. 4.3e-15;  
Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDHFEEVFNVPSCISNNPTCWAICKRIPNKKPGKK 49  
|| |||||:||| ||||||||||||||||||||||||||||||||  
Db 149 KRSKNPKPKPDYHFEVFNVPSCIGNQLCKSICKTIPSINKPDKK 197

RESULT 11

MGN260

major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)

N;Alternate names: attachment glycoprotein G

C;Species: human respiratory syncytial virus

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Jul-1999

C;Accession: A37077

R;Sullender, W.M.; Anderson, K.; Wertz, G.W.  
Virology 178, 195-203, 1990

A;Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis  
gous subgroup virus challenge.

A;Reference number: A37077; PMID:90357765

A;Accession: A37077

A:Molecule type: mRNA

A:Residues: 1-292 <SUL>

A:CROSS-references: EMBL:M55633; NID:g333944; PIDN:AAA47413.1; PID:g333945

C;Genetics:

A:Gene: G

C;Superfamily: respiratory syncytial virus major surface glycoprotein G

C;Keywords: glycoprotein; transmembrane protein

F:43-63/Domain: transmembrane #status predicted <TMN>

F:81,86,100,230,290/Binding site: carbohydrate (Asn) #status predicted

Query Match 66.0%; Score 190; DB 1; Length 292;  
Best Local Similarity 65.3%; Pred. No. 4.3e-15;  
Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 21, 2001, 14:15:36 ; Search time 8.11 seconds  
(without alignments)  
206.969 Million cell updates/sec

Title: US-09-202-035-1

Perfect score: 288

Sequence: 1 KORQNKPPSKPNDFHFEV.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	288	100.0	298	1	VGLG_HRSVA
2	285	99.0	297	1	VGLG_HRSV2
3	285	99.0	297	1	VGLG_HRSV3
4	285	99.0	297	1	VGLG_HRSV6
5	285	99.0	298	1	VGLG_HRSV5
6	280	97.2	298	1	VGLG_HRSV1
7	279	96.9	297	1	VGLG_HRSV4
8	273	94.8	297	1	VGLG_HRSV7
9	190	66.0	292	1	VGLG_HRSV1
10	190	66.0	292	1	VGLG_HRSV8
11	83.5	29.0	257	1	VGLG_BRSCV
12	80	27.8	263	1	VGLG_BRSCV2
13	77.5	26.9	257	1	VGLG_BRSCV
14	77.5	26.9	263	1	VGLG_BRSCVW
15	77.5	26.9	263	1	VGLG_ORSCV
16	76.5	26.6	263	1	VGLG_BRSV1
17	76.5	26.6	263	1	VGLG_BRSV4
18	74	25.7	257	1	VGLG_BRSCV
19	74	25.7	257	1	VGLG_BRSCV2
20	73	25.3	257	1	VGLG_BRSCV7
21	66.5	23.1	198	1	DAPE_YERPE
22	66.5	23.1	274	1	DAPE_ECOLI
23	64	22.2	37	1	SCK3_LEIQH
24	63.5	22.0	274	1	DAPE_HAEIN
25	62	21.5	37	1	SCK3_LEIQH
26	58.5	20.3	276	1	DAPE_PSEAE
27	57.5	20.0	276	1	DAPE_PSEFL
28	57	19.8	279	1	DAPE_AQAE
29	56.5	19.6	748	1	JSB1_TRINI
30	55.5	19.3	747	1	SSP1_BOMMO
31	55	19.1	35	1	SCKK_TITSE
32	54.5	18.9	902	1	SYGI_YEAST
33	54	18.8	160	1	LSPA_BUCAI

RESULT	1	VGLG_HRSVA	STANDARD;	PRT;	298 AA.
AC	P03423;				
DC	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1998 (Rel. 36, Last annotation update)				
DE	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).				
GN	G.				
OS	Human respiratory syncytial virus (strain A2).				
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;				
OC	Paramyxoviridae; Pneumovirinae; Pneumovirus.				
OX	NCBI_TaxID=11259;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85216636; PubMed=3858865;				
RA	Wertz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.;				
RT	"Nucleotide sequence of the G protein gene of human respiratory syncytial virus reveals an unusual type of viral membrane protein.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86067198; PubMed=4069997;				
RA	Satake M., Colligan J.E., Elango N., Norrby E., Venkatesan S.;				
RT	"Respiratory syncytial virus envelope glycoprotein (G) has a novel structure.";				
RL	Nucleic Acids Res. 13:7795-7812(1985).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95266253; PubMed=7747420;				
RA	Connors M., Crowe J.E. Jr., Firestone C.Y., Murphy B.R., Collins P.L.;				
RT	"A cold-passaged, attenuated strain of human respiratory syncytial virus contains mutations in the F and L genes.";				
RL	Virology 208:478-484(1995).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97187925; PubMed=90353372;				
RA	Crowe J.E. Jr., Firestone C.Y., Whitehead S.S., Collins P.L., Murphy B.R.;				
RT	"Acquisition of the ts phenotype by a chemically mutagenized cold-passaged human respiratory syncytial virus vaccine candidate results from the acquisition of a single mutation in the polymerase (L) gene.";				
RL	Virus Genes 13:269-273(1996).				
CC	-1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTININATING ACTIVITIES.				
CC	-1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.				
CC	-1- PFM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.				
CC	-----				
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34	53.5	18.6	237	1	HK31_MOUSE	p97436	mus musculus
35	52.5	18.2	284	1	DAPE_BUCAI	p57649	buchnera ap
36	52.5	18.2	360	1	MTSB_LALCI	p34878	lactococcus
37	52	18.1	102	1	VE7_PAPVE	p11332	european el
38	52	18.1	454	1	TNRI_MOUSE	p25118	mus musculus
39	52	18.1	2386	1	RAD3_SCHPO	Q02099	schizosacch
40	51.5	17.9	354	1	MBHS_WOLSU	p31884	wollinella s
41	51	17.7	36	1	SCK3_LEIQH	p45660	leirus qui
42	51	17.7	118	1	YK07_YEAST	p32858	saccharomyc
43	51	17.7	245	1	YIT8_YEAST	p40574	saccharomyc
44	51	17.7	675	1	PRTS_MOUSE	C08761	mus musculus
45	51	17.7	1059	1	CERU_RAT	P13635	rattus norv

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CC -----  
 DR EMBL; M11486; AAB59857.1; -  
 DR EMBL; X03149; CAA26928.1; -  
 DR EMBL; U50362; AAB86663.1; -  
 DR EMBL; U50363; AAB86675.1; -  
 DR EMBL; U63644; AAC55969.1; -  
 DR PIR; A04039; MGNZ.  
 DR InterPro; IPR000925; -  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 KW Transmembrane; Glycoprotein.  
 FT DOMAIN 1 37  
 FT TRANSMEM 38 66  
 FT DOMAIN 67 298  
 FT CARBOHYD 135 135  
 FT CARBOHYD 237 237  
 FT CARBOHYD 251 251  
 FT CARBOHYD 251 251  
 SQ SEQUENCE 298 AA; 32586 MW; 993C3D2DD68BC634 CRC64;

Query Match 100.08; Score 288; DB 1; Length 298;

Best Local Similarity 100.08; Pred. No. 1.1e-26;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKK 49  
 Db 149 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKK 197

RESULT 2

ID VGLG\_HRSV2  
 AC P27021; STANDARD; PRT; 297 AA.  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-AUG-1992 (Rel. 23, Last annotation update)  
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
 GN G.  
 OS Human respiratory syncytial virus (strain rsb642).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11252;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91374005; PubMed=1895054;  
 RA Cane P.A., Matthews D.A., Pringle C.R.;  
 RT "Identification of variable domains of the attachment (G) protein of  
 subgenus A respiratory syncytial viruses.";  
 RL J. Gen. Virol. 72:2091-2096(1991).  
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
 CC HEMAGGLUTININATING ACTIVITIES.  
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
 CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS  
 CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.  
 DR PIR; J01204; J01204.  
 DR InterPro; IPR000925; -  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 KW Transmembrane; Glycoprotein.  
 FT DOMAIN 1 37  
 FT TRANSMEM 38 66  
 FT DOMAIN 67 297  
 FT CARBOHYD 135 135  
 FT CARBOHYD 144 144  
 FT CARBOHYD 237 237  
 FT CARBOHYD 251 251  
 SQ SEQUENCE 297 AA; 32745 MW; FC72A7F3A8EBF67C CRC64;

Query Match 99.08; Score 285; DB 1; Length 297;  
 Best Local Similarity 98.08; Pred. No. 2.4e-26;

Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKK 49  
 Db 149 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKR 197

RESULT 3

VGLG\_HRSV3  
 ID VGLG\_HRSV3 STANDARD; PRT; 297 AA.  
 AC P27022;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-AUG-1992 (Rel. 23, Last annotation update)  
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
 GN G.  
 OS Human respiratory syncytial virus (strain rsb1734).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11253;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91374005; PubMed=1895054;  
 RA Cane P.A., Matthews D.A., Pringle C.R.;  
 RT "Identification of variable domains of the attachment (G) protein of  
 subgenus A respiratory syncytial viruses.";  
 RL J. Gen. Virol. 72:2091-2096(1991).  
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
 CC HEMAGGLUTININATING ACTIVITIES.  
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
 CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS  
 CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.  
 DR PIR; J01205; J01205.  
 DR InterPro; IPR000925; -  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 KW Transmembrane; Glycoprotein.  
 FT DOMAIN 1 37  
 FT TRANSMEM 38 66  
 FT DOMAIN 67 297  
 FT CARBOHYD 135 135  
 FT CARBOHYD 237 237  
 FT CARBOHYD 251 251  
 FT CARBOHYD 251 251  
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Query Match 99.08; Score 285; DB 1; Length 297;  
 Best Local Similarity 98.08; Pred. No. 2.4e-26;  
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKK 49  
 Db 149 KORQKPPSKPNDFFHFVFPVCSICSNPTCWAICKRIPNKKPGKR 197

RESULT 4

VGLG\_HRSV6  
 ID VGLG\_HRSV6 STANDARD; PRT; 297 AA.  
 AC P27025;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-AUG-1992 (Rel. 23, Last annotation update)  
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
 GN G.  
 OS Human respiratory syncytial virus (strain rsb6256).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11256;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91374005; PubMed=1895054;  
 RA Cane P.A., Matthews D.A., Pringle C.R.;

DR	InterPro: IPR000925; -
DR	Pfam: PF00802; Glycoprotein_G; 1.
KW	Transmembrane; Glycoprotein.
FT	DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 38 66 POTENTIAL.
FT	DOMAIN 67 298 EXTRACELLULAR (POTENTIAL).
FT	CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 250 250 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE 298 AA; 32781 MW; B79FEFA4B4A73B0E CRC64;
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Best Local Similarity 98.0%; Pred. No. 2.4e-26;	
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Db	149 KORQKPPKNPNDFHFEVFNFPSCISNPNPTCWAICKRIPNKKPGKK 197
RESULT 6	
VGLG_HRSVS	
ID VGLG_HRSVS STANDARD; PRT; 298 AA.	
AC P27024;	
DT 01-AUG-1992 (Rel. 23, Created)	
DT 01-AUG-1992 (Rel. 23, Last sequence update)	
DE 30-MAY-2000 (Rel. 39, Last annotation update)	
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).	
GN G.	
OS Human respiratory syncytial virus (strain rsb6190).	
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;	
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.	
OX NCBI_TaxID=11255;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=91374005; PubMed=1895054;	
RA Cane P.A., Matthews D.A., Pringle C.R.;	
RT "Identification of variable domains of the attachment (G) protein of	
RL subgroup A respiratory syncytial viruses.";	
RL J. Gen. Virol. 72:2091-2096(1991).	
CC -I- FUNCTION: UNLIKE THE OTHER PARAMYOXIVIRUS ATTACHMENT PROTEINS, THE	
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND	
CC HEMAGGLUTINATING ACTIVITIES.	
CC -I- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED	
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.	
CC -I- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS	
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.	
DR PIR; JQ1207; JQ1207.	
DR InterPro: IPR000925; -	
DR Pfam: PF00802; Glycoprotein_G; 1.	
KW Transmembrane; Glycoprotein.	
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).	
FT TRANSMEM 38 66 POTENTIAL.	
FT DOMAIN 67 298 EXTRACELLULAR (POTENTIAL).	
FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).	
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).	
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).	
FT CARBOHYD 250 250 N-LINKED (GLCNAC. .) (POTENTIAL).	
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).	
SQ SEQUENCE 298 AA; 32769 MW; 4D74E854D34D7BA5 CRC64;	
Query Match 97.2%; Score 280; DB 1; Length 298;	
Best Local Similarity 95.9%; Pred. No. 9.1e-26;	
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
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Db	149 KORQKPPKNPNDFHFEVFNFPSCISNPNPTCWAICKRIPNKKPGKK 197

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RESULT 7
VGLG_HRSV4
ID VGLG_HRSV4 STANDARD; PRT; 297 AA.
AC P27023;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
GN G.
OS Human respiratory syncytial virus (strain rsb5857).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
  subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
  HEMAGGLUTININATING ACTIVITIES.
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
  CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
  DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
DR PIR; J01206; J01206.
DR InterPro; IPR000925; -.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 297 AA; 32772 MW; 10488CCA475936BE CRC64;

Query Match 96.9%; Score 279; DB 1; Length 297;
Best Local Similarity 95.9%; Pred. No. 1.2e-25;
Matches 47; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 149 KORQKPPSKNDFHFEVFNFCISNNPTCWAICKRIPNKKPGKK 197

RESULT 8
VGLG_HRSV7
ID VGLG_HRSV7 STANDARD; PRT; 297 AA.
AC P27026;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
GN G.
OS Human respiratory syncytial virus (strain rsb6614).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11257;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
  subgroup A respiratory syncytial viruses.";

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J. Gen. Virol. 72:2091-2096(1991).
-1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
  HEMAGGLUTININATING ACTIVITIES.
-1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
  CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
  DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
DR PIR; J01209; J01209.
DR InterPro; IPR000925; -.
DR Pfam; PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 297 AA; 32670 MW; 58B384028E437ACD CRC64;

Query Match 94.8%; Score 273; DB 1; Length 297;
Best Local Similarity 93.9%; Pred. No. 5.9e-25;
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 149 KORQKPPSKNDFHFEVFNFCISNNPTCWAICKRIPNKKPGKK 197

RESULT 9
VGLG_HRSV1
ID VGLG_HRSV1 STANDARD; PRT; 292 AA.
AC P20896;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).
GN G.
OS Human respiratory syncytial virus (subgroup B / strain 18537).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11251;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289657; PubMed=2441388;
RA Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
RT "The G glycoprotein of human respiratory syncytial viruses of
  subgroups A and B: extensive sequence divergence between
  antigenically related proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
  HEMAGGLUTININATING ACTIVITIES.
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
  CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
  DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M17213; AAA47412.1; -.
CC PIR; B32703; MGWZ18.
CC InterPro; IPR000925; -.
CC Pfam; PF00802; Glycoprotein_G; 1.

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KW Transmembrane; Glycoprotein.  
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 38 66 POTENTIAL.  
 FT DOMAIN 67 292 EXTRACELLULAR (POTENTIAL).  
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 292 AA; 32306 MW; BC8C59F69CA7AFC2 CRC64;

Query Match 66.0%; Score 190; DB 1; Length 292;  
 Best Local Similarity 65.3%; Pred. No. 2.7e-15;  
 Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Oy 1 KQONKPPSKPNDFHFEVFNPCISGNNPTCAICKRIPNKKPKKK 49  
 Db 149 KSRKNPKPKDDYHFEVFNPCISGNNQCKSICKTIPSNKPKKK 197

RESULT 10  
 VGLG\_HRSV8 STANDARD; PRT; 292 AA.  
 AC P23041;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-AUG-1992 (Rel. 23, Last annotation update)  
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
 GN G.  
 OS Human respiratory syncytial virus (subgroup B / strain 8/60).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11258;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90357765; PubMed=1697126;  
 RA Sullender W.M., Anderson K., Wertz G.W.;  
 RT "The respiratory syncytial virus subgroup B attachment glycoprotein:  
 RT analysis of sequence, expression from a recombinant vector, and  
 RT evaluation as an immunogen against homologous and heterologous  
 RT subgroup virus challenge.";  
 RL Virology 178:195-203(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91374595; PubMed=1895391;  
 RA Sullender W.M., Mufson M.M., Anderson L.J., Wertz G.W.;  
 RT "Genetic diversity of the attachment protein of subgroup B  
 RT respiratory syncytial viruses.";  
 RL J. Virol. 65:5425-5434(1991).  
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
 CC HEMAGGLUTININATING ACTIVITIES.  
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
 CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS  
 CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.  
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 CC  
 CC EMBL; M55633; AAA47413.1; -  
 CC EMBL; M73545; AAA47408.1; -  
 CC PIR; A37077; MGNZ60.  
 DR InterPro; IPR000925; -  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 KW Transmembrane; Glycoprotein.  
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 38 66 POTENTIAL.  
 FT DOMAIN 67 292 EXTRACELLULAR (POTENTIAL).

FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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Query Match 66.0%; Score 190; DB 1; Length 292;  
 Best Local Similarity 65.3%; Pred. No. 2.7e-15;  
 Matches 32; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Oy 1 KQONKPPSKPNDFHFEVFNPCISGNNPTCAICKRIPNKKPKKK 49  
 Db 149 KSRKNPKPKDDYHFEVFNPCISGNNQCKSICKTIPSNKPKKK 197

RESULT 11  
 VGLG\_BRVSVC STANDARD; PRT; 257 AA.  
 AC P22261;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
 GN G.  
 OS Bovine respiratory syncytial virus (strain Copenhagen) (BRS).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11248;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91012801; PubMed=2214024;  
 RA Lerch R.A., Anderson K., Wertz G.W.;  
 RT "Nucleotide sequence analysis and expression from recombinant vectors  
 RT demonstrate that the attachment protein G of bovine respiratory  
 RT syncytial virus is distinct from that of human respiratory syncytial  
 RT virus.";  
 RL J. Virol. 64:5559-5569(1990).  
 RN [2]  
 RP STRUCTURE BY NMR OF 158-189.  
 RC STRAIN=391-2;  
 RX MEDLINE=97098087; PubMed=8942628;  
 RA Doreleijers J.F., Langedijk J.P.M., Haard K., Boelens R.,  
 RA Rullmann J.A., Schaaper W.M., van Oirschot J.T., Kaptein R.;  
 RT "Solution structure of the immunodominant region of protein G of  
 RT bovine respiratory syncytial virus.";  
 RL Biochemistry 35:14684-14688(1996).  
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
 CC HEMAGGLUTININATING ACTIVITIES.  
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
 CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B  
 CC HRS VIRUS.  
 CC  
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 CC  
 CC EMBL; M58307; AAA42810.1; -  
 CC PIR; A36408; MGNZBR.  
 DR PDB; 1BRV; 05-JUN-97.  
 DR InterPro; IPR000925; -  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 KW Transmembrane; Glycoprotein; 3D-structure.  
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 38 66 POTENTIAL.  
 FT DOMAIN 67 257 POTENTIAL.  
 FT DISULFID 173 186 EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 176 182



DE GN MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
 OS Bovine respiratory syncytial virus (strain Whb) (BRV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=82825;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97288324; PubMed=9143302;  
 RA Furze J., Roberts S., Wertz G., Taylor G.;  
 RT "Antigenically distinct G glycoproteins of BRV strains share a high  
 degree of genetic homogeneity.";  
 RL Virology 231:48-58(1997).  
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
 CC HEMAGGLUTININATING ACTIVITIES.  
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
 CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B  
 CC HRS VIRUS.  
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 CC -----  
 DR EMBL; Y08717; CA69967.1; .  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; .  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 KW Transmembrane; Glycoprotein.  
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 38 66 POTENTIAL.  
 FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 173 186 BY SIMILARITY.  
 FT DISULFID 176 182 BY SIMILARITY.  
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 263 AA; 29050 MW; 0D06AF7FCB46B858 CRC64;  
 Query Match 26.9%; Score 77.5; DB 1; Length 263;  
 Best Local Similarity 29.0%; Pred. No. 0.031;  
 Matches 20; Conservative 5; Mismatches 19; Indels 25; Gaps 3;  
 QY 6 KPSPKP-----NNDFH--FEVFNVPSCISNNPTCWAIC-----KR 40  
 DB 145 KPPINPGSNPENQHDHNSQTLPHVPCSTCEGNPCSSLCQIGPERASSRAPITILKK 204  
 QY 41 IPNKKPGKK 49  
 DB 205 TPKPKTKK 213  
 RESULT 15  
 VGLG\_ORSVW  
 ID VGLG\_ORSVW STANDARD; PRT; 263 AA.  
 AC Q86695;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G).  
 GN G.  
 OS Bovine respiratory syncytial virus (strain WSU 83-1578) (ORSV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=79699;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=94103788; PubMed=8277288;  
 RA Mallipeddi S.K., Samal S.K.;  
 RT "Analysis of the ovine respiratory syncytial virus (RSV) G  
 glycoprotein gene defines a subgroup of ungulate RSV.";  
 RL J. Gen. Virol. 74:2787-2791(1993).  
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE  
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND  
 CC HEMAGGLUTININATING ACTIVITIES.  
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED  
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
 CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B  
 CC HRS VIRUS.  
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 CC -----  
 DR EMBL; S67863; AAB29551.1; .  
 DR EMBL; S67862; AAB29551.1; JOINED.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; .  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 KW Transmembrane; Glycoprotein.  
 FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 38 66 POTENTIAL.  
 FT DOMAIN 67 263 EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 173 186 BY SIMILARITY.  
 FT DISULFID 176 182 BY SIMILARITY.  
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 263 AA; 29225 MW; 81A649C6047B3B71 CRC64;  
 Query Match 26.9%; Score 77.5; DB 1; Length 263;  
 Best Local Similarity 25.8%; Pred. No. 0.031;  
 Matches 17; Conservative 10; Mismatches 18; Indels 21; Gaps 2;  
 QY 4 QNKPKSPKNNDF--HFEVFNVPSCISNNPTCWAIC-----KKRP 42  
 DB 151 QKSNPSEIQQDYSDFOILPYVPCNICEGDSACLSLCQDRSESLDKALTTTPKTPKPM 210  
 QY 43 NKKPGK 48  
 DB 211 TKKPTK 216  
 Search completed: May 21, 2001, 14:17:12  
 Job time: 96 sec



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OM protein - protein search, using sw model

Run on: May 21, 2001, 14:15:22 ; Search time 19.45 Seconds  
(without alignments)  
295.280 Million cell updates/sec

Title: US-09-202-035-1  
Perfect score: 288  
Sequence: 1 KORQNKPSKPNDFHFVFN.....NNPTCWAICKRIPNKKPGKK 49

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL15.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp-organelle.\*  
9: sp-phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_unclassified.\*  
13: sp\_vertebrate.\*  
14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	288	100.0	293 14 Q9YVB3
2	285	99.0	278 14 Q9Q6U1
3	285	99.0	278 14 Q9Q6T7
4	285	99.0	278 14 Q9Q6T4
5	285	99.0	278 14 Q9Q6T3
6	285	99.0	278 14 Q9Q6T0
7	285	99.0	279 14 Q9Q6U0
8	285	99.0	279 14 Q9Q6T9
9	285	99.0	279 14 Q9Q6T8
10	285	99.0	279 14 Q9Q6T5
11	285	99.0	279 14 Q9Q6T2
12	285	99.0	279 14 Q9Q6S9
13	285	99.0	279 14 Q9Q6S7
14	285	99.0	279 14 Q9Q6S6
15	285	99.0	279 14 Q9Q6S0
16	285	99.0	279 14 Q9Q6R9
17	285	99.0	292 14 Q9YVB2
18	285	99.0	292 14 Q9YVB0
19	285	99.0	295 14 Q86356

20	285	99.0	295	14	Q86359	Q86359	respiratory
21	285	99.0	295	14	Q86360	Q86360	respiratory
22	285	99.0	297	14	Q82057	Q82057	human respi
23	285	99.0	297	14	Q82058	Q82058	human respi
24	285	99.0	297	14	Q82066	Q82066	human respi
25	285	99.0	297	14	Q82067	Q82067	human respi
26	285	99.0	297	14	Q82071	Q82071	human respi
27	285	99.0	297	14	Q82074	Q82074	human respi
28	285	99.0	297	14	Q82078	Q82078	human respi
29	285	99.0	297	14	Q9YVB5	Q9YVB5	human respi
30	285	99.0	297	14	Q82065	Q82065	human respi
31	285	99.0	298	14	Q82068	Q82068	human respi
32	285	99.0	298	14	Q82073	Q82073	human respi
33	285	99.0	298	14	Q09634	Q09634	human respi
34	285	99.0	298	14	Q09719	Q09719	respiratory
35	285	99.0	298	14	Q01929	Q01929	human respi
36	280	97.2	279	14	Q9Q6S8	Q9Q6S8	human respi
37	280	97.2	293	14	Q9YVB1	Q9YVB1	human respi
38	280	97.2	296	14	Q86358	Q86358	respiratory
39	280	97.2	297	14	Q91944	Q91944	human respi
40	280	97.2	298	14	Q82056	Q82056	human respi
41	280	97.2	298	14	Q82060	Q82060	human respi
42	280	97.2	298	14	Q82061	Q82061	human respi
43	280	97.2	298	14	Q82062	Q82062	human respi
44	280	97.2	298	14	Q82075	Q82075	human respi
45	280	97.2	298	14	Q82076	Q82076	human respi

ALIGNMENTS

RESULT 1	
Q9YVB3	
ID Q9YVB3	PRELIMINARY; PRT: 293 AA.
AC Q9YVB3;	
DT 01-MAY-1999	(TREMBLrel. 10, Created)
DT 01-MAY-1999	(TREMBLrel. 10, Last sequence update)
DT 01-MAY-2000	(TREMBLrel. 13, Last annotation update)
DE ATTACHMENT	GLYCOPROTEIN G (FRAGMENT).
OS Human	respiratory syncytial virus.
OC Viruses;	ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae;	Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;	
RN [1]	
RP SEQUENCE	FROM N.A.
RC STRAIN-WV6973;	
RX MEDLINE=9022964;	PubMed=9806017;
RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;	
RT "Antigenic and genetic diversity among the attachment proteins of	
RT group A respiratory syncytial viruses that have caused repeat	
RT infections in children."	
RL J. Infect. Dis. 178:925-932(1998).	
DR EMBL; AF065407; AAD02943.1; -	
DR INTERPRO; IPR000255; -	
DR INTERPRO; IPR002965; -	
DR PFAM; PF00802; Glycoprotein_G; 1.	
DR PRINTS; PR01217; PRICHEXTENS.	
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.	
FT NON_TER	1
SQ SEQUENCE	293 AA; 32125 MW; 1775B43396A63CCF CRC64;

Query Match	100.0%;	Score 288;	DB 14;	Length 293;
Best Local Similarity	100.0%;	Pred. NO. 4.5e-30;		
Matches 49;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	KORQNKPSKPNDFHFVFN	VFVFN	VFVFN	VFVFN
Db 144	KORQNKPSKPNDFHFVFN	VFVFN	VFVFN	VFVFN

RESULT 2

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Q906U1      PRELIMINARY;      PRT;      278 AA.
ID Q906U1;
AC Q906U1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91142;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193305; AAF23728.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR INTERPRO; IPR002965; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30461 MW; AC113DCCCF47EDE CRC64;

Query Match      99.0%; Score 285; DB 14; Length 278;
Best Local Similarity 98.0%; Pred. No. 1.le-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPSKPNDDHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 49
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KORQNKPPKNDDHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 3
Q906T7      PRELIMINARY;      PRT;      278 AA.
ID Q906T7;
AC Q906T7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92308;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193309; AAF23732.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR INTERPRO; IPR002965; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30548 MW; B33F085F99E1A9D0 CRC64;

Query Match      99.0%; Score 285; DB 14; Length 278;
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Best Local Similarity 98.0%; Pred. No. 1.le-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPSKPNDDHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 49
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Db 130 KORQNKPPKNDDHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 4
Q906T4      PRELIMINARY;      PRT;      278 AA.
ID Q906T4;
AC Q906T4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92528;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193312; AAF23735.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR INTERPRO; IPR002965; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30474 MW; 2E05963863BF8A75 CRC64;

Query Match      99.0%; Score 285; DB 14; Length 278;
Best Local Similarity 98.0%; Pred. No. 1.le-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQNKPSKPNDDHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 49
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KORQNKPPKNDDHFEVFNVPSCSICSNPTCWAICKRIPNKKPGKK 178

RESULT 5
Q906T3      PRELIMINARY;      PRT;      278 AA.
ID Q906T3;
AC Q906T3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=93006;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193313; AAF23736.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
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RC	STRAIN-91242;
RA	Choi E.H., Lee H.J.;
RT	"Genetic diversity and molecular epidemiology of the G protein of subgroup A and B respiratory syncytial viruses isolated over nine consecutive epidemics.";
RL	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF193306; AAF23729.1; -;
DR	INTERPRO; IPR000255; -;
DR	INTERPRO; IPR000925; -;
DR	PFAM; PF0802; Glycoprotein_G; 1.
DR	PROSITE; PS00012; PHOSPHOPANTHETINE; UNKNOWN_1.
FT	NON_TER
SQ	SEQUENCE 279 AA; 30544 MW; 6B270AEB1CB3533 CRC64;
Query Match	99.0%; Score 285; DB 14; Length 279;
Best Local Similarity	98.0%; Pred. No. 1.le-29;
Matches	48; Conservative 1; Mismatches 0; Indels 0; Caps 0;
Qy	1 KORQNKPSPKPNDFHFVFVPCISCSNNPTCWAICKRIPNKKPGKK 49      :     :     :     :     :     :     :
Db	130 KORQNKPKNPNDHFHFVFVPCISCSNNPTCWAICKRIPNKKPGKK 178
RESULT	8
Q906T9	PRELIMINARY; PRT; 279 AA.
ID	AC Q906T9;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE	GLYCOPROTEIN (FRAGMENT).
G.	
OS	Human respiratory syncytial virus.
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC	Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX	NCBI_TaxID=11250;
[1]	
RN	SEQUENCE FROM N.A.
RP	
RC	STRAIN-91399;
RA	Choi E.H., Lee H.J.;
RT	"Genetic diversity and molecular epidemiology of the G protein of subgroup A and B respiratory syncytial viruses isolated over nine consecutive epidemics.";
RL	Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF193307; AAF23730.1; -;
DR	INTERPRO; IPR000255; -;
DR	INTERPRO; IPR000925; -;
DR	PFAM; PF0802; Glycoprotein_G; 1.
DR	PRINTS; PR01217; PRICHEXTENS.
DR	PROSITE; PS00012; PHOSPHOPANTHETINE; UNKNOWN_1.
FT	NON_TER
SQ	SEQUENCE 279 AA; 30570 MW; AB6CF9CD8F8A97C CRC64;
Query Match	99.0%; Score 285; DB 14; Length 279;
Best Local Similarity	98.0%; Pred. No. 1.le-29;
Matches	48; Conservative 1; Mismatches 0; Indels 0; Caps 0;
Qy	1 KORQNKPSPKPNDFHFVFVPCISCSNNPTCWAICKRIPNKKPGKK 49      :     :     :     :     :     :     :
Db	130 KORQNKPKNPNDHFHFVFVPCISCSNNPTCWAICKRIPNKKPGKK 178
RESULT	9
Q906T8	PRELIMINARY; PRT; 279 AA.
ID	AC Q906T8;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE	GLYCOPROTEIN (FRAGMENT).

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GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92011;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193308; AAF23731.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30499 MW; 4E1CDF2F7E569E3A CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;
Best Local Similarity 98.0%; Pred. No. 1.le-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGKK 49
DB 130 KORQKPPKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGKK 178

RESULT 10
QY Q06T5 PRELIMINARY; PRT; 279 AA.
AC Q06T5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92415;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193311; AAF23734.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30442 MW; F53F5932FCE77E89 CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;
Best Local Similarity 98.0%; Pred. No. 1.le-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGKK 49
DB 130 KORQKPPKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGKK 178

RESULT 11

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QY Q06T2 PRELIMINARY; PRT; 279 AA.
AC Q06T2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=93057;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193314; AAF23737.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30547 MW; 86DFD42DC8A8F500 CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;
Best Local Similarity 98.0%; Pred. No. 1.le-29;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORQKPPSKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGKK 49
DB 130 KORQKPPKPNDFHFEVFNPCISCSNNPTCWAICKRIPNKKPGKK 178

RESULT 12
QY Q06S9 PRELIMINARY; PRT; 279 AA.
AC Q06S9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95026;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroup A and B respiratory syncytial viruses isolated over nine
RT consecutive epidemics.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF193317; AAF23740.1; -
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000925; -
DR PFAM; PF00802; Glycoprotein_G; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 279 AA; 30529 MW; AEC4D787983D472D CRC64;

Query Match 99.0%; Score 285; DB 14; Length 279;

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DR	INTERPRO; IPR002965; -.	
DR	PFAM; PF00802; Glycoprotein_G; 1.	
DR	PRINTS; PR01217; PRICHEXTENS.	
DR	PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.	
DR	NON_TER	1
FT	SEQUENCE	279 AA; 30445 MW; F4D236EE8E694A9E CRC64;

	Query Match	99.0%	Score 285;	DB 14;	Length 276
	Best Local Similarity	98.0%;	Pred. No. 1.le-29;		
	Matches	48; Conservative	1; Mismatches	0;	Indels
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QY	I KQRKNPKSPKNNDDFFHEFVFNVPVCISCSNPNPTCAWICKRIPNKPPGKK	49			
DH	LQQQLPSSDPSKPDNDDEEVEVFPCSTSCSNPTCAWICRPNNKPGRGG	178			

DR INTERPRO: IPR000325; -;  
DR INTERPRO: IPR000325; -;  
DR INTERPRO: IPR002965; -;  
DR PFAM: PF00802; Glycoprotein\_G; 1.  
DR PRINTS: PRO1217; PRICHEXTENS.  
DR PROSITE: PS00012; PHOSPHOANTHETHEINE; UNKNOWN\_1.  
DR NON\_TER: 1  
DR SEQUENCE 279 AA: 30467 MW: 8943C99707A9DB47 CRC64:  
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Search completed: May 21, 2001, 14:17:00  
Job time: 98 sec

